

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 29, 2004, 18:16:47 ; Search time 23 Seconds  
(without alignments)  
1207.599 Million cell updates/sec

Title: US-09-892-360-2  
Perfect score: 2760  
Sequence: 1 MPFLYTDPLSLVAVPAAP.....IPTDTKDRPENNSLLEDN 538

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/2/iaa/5A COMB.pcp.\*
- 2: /cgn2\_6/prodata/2/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/prodata/2/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/prodata/2/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/prodata/2/iaa/6CTUS COMB.pcp.\*
- 6: /cgn2\_6/prodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248.5	45.2	411	3	US-09-236-080-6
2	1242.5	45.0	411	3	US-09-236-080-2
3	1242.5	45.0	411	4	US-09-336-643A-83
4	1238.5	44.9	370	4	US-09-144-914-8
5	812.5	29.4	393	4	US-09-432-470-2
6	812.5	29.4	393	4	US-09-432-470-4
7	483	17.5	499	4	US-09-561-763-2
8	483	17.5	499	4	US-09-431-367B-2
9	447	16.2	107	3	US-09-236-080-4
10	403	14.6	336	3	US-08-749-816-2
11	403	14.6	336	4	US-09-144-914-2
12	396	14.3	332	4	US-09-561-763-5
13	396	14.3	332	4	US-09-431-367B-5
14	361	13.1	361	4	US-09-362-842-14
15	352.5	12.8	405	4	US-09-144-914-5
16	349.5	12.7	394	4	US-09-144-914-4
17	333.5	12.1	333	4	US-09-336-643A-81
18	333.5	12.1	333	4	US-09-561-763-8
19	333.5	12.1	333	4	US-09-431-367B-8
20	323	11.7	408	4	US-09-362-842-12
21	290.5	10.5	618	1	US-08-332-312-2
22	233.5	8.5	995	4	US-09-362-842-2
23	233	8.4	395	4	US-08-362-842-6
24	220	8.0	401	4	US-09-561-763-11
25	220	8.0	401	4	US-09-431-367B-11
26	212.5	7.7	336	1	US-08-332-312-4
27	197	7.1	730	4	US-09-362-842-4

28	197	7.1	741	4	US-09-362-842-67	Sequence 67, Appl
29	186.5	6.8	1153	4	US-09-362-842-8	Sequence 8, Appl
30	164.5	6.0	347	3	US-08-749-816-3	Sequence 3, Appl
31	164.5	6.0	347	4	US-09-144-914-6	Sequence 6, Appl
32	159	5.8	383	3	US-08-749-816-4	Sequence 4, Appl
33	159	5.8	383	4	US-09-144-914-7	Sequence 7, Appl
34	137.5	5.0	146	4	US-09-362-842-69	Sequence 69, Appl
35	134	4.9	197	4	US-09-336-643A-16	Sequence 16, Appl
36	126.5	4.6	989	4	US-08-694-777A-4	Sequence 4, Appl
37	125	4.5	677	4	US-09-177-650-4	Sequence 4, Appl
38	123.5	4.5	962	4	US-09-614-480-9	Sequence 9, Appl
39	123.5	4.5	962	4	US-09-694-777A-3	Sequence 3, Appl
40	118.5	4.3	446	4	US-10-162-012-8	Sequence 8, Appl
41	118.5	4.3	676	3	US-09-135-021-2	Sequence 2, Appl
42	118.5	4.3	676	3	US-09-135-020-2	Sequence 2, Appl
43	118.5	4.3	676	3	US-09-135-010A-2	Sequence 2, Appl
44	118.5	4.3	676	4	US-09-444-871-2	Sequence 2, Appl
45	118.5	4.3	676	4	US-09-634-920-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-236-080-6  
; Sequence 6, Application US/09236080  
; Patent No. 6242217  
; GENERAL INFORMATION:  
; APPLICANT: Helen Meadows  
; APPLICANT: Conrad Chapman  
; TITLE OF INVENTION: No. 6242217el Compounds  
; FILE REFERENCE: GP30031  
; CURRENT APPLICATION NUMBER: US/09/236.080  
; CURRENT FILING DATE: 1999-01-25  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 411  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-236-080-6

Query Match	45.2%	Score	1248.5	DB	3	Length	411
Best Local Similarity	64.3%	Pred. No.	9.6e-107				
Matches	247	Conservative	53	Mismatches	67	Indels	17
Gaps	5						
Qy	17	AAAPVCPKSNATGQPAPAPPTPTPLSLSSRATVVA-RMEGTSGGLQTVNKKTVVAI	75				
Db	2	AAPDLLDPKSA-----AQNKRPLSFSSKPTVLASRVESDS---AINVMKKTVSTI	50				
Qy	76	FVVVVVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQOELETHIQALDAD	135				
Db	51	FLVVVLYLIIGAANVFKALEQPOEISQRTTIVIQQTFFIAQHACVNSTELDELIQQIVAAI	110				
Qy	136	NAGVSPGNSSNNSHWDLSGAFFAGVTITIGVNIAPSTEGKIFCIYVAFIPFLF	195				
Db	111	NAGIPLGNSSNQSHWDLSGFFAGVTITIGVNIAPSTEGKIFCIYVAFIPFLF	170				
Qy	136	GFLLAGIGDQGTIFGKSIARVEKVRKQVQSOTKIRVISTILFILACIVFVTPAVIF	255				
Db	171	GFLLAGVGDQGTIFGKIAKVEDTFIKWNVSQTKIRIISTITIFLFGCVLFVALPAVIF	230				
Qy	256	KYIEGWTALSIYVWVTLTTVGGDFVAGGNAGINREWKPLVFWFVILGLAYFAVL	315				
Db	231	KHIEGWSALDAIFVVTITLTIGFDYVAGG-SDEYLDIFYKPVVWFVILGLAYFAVL	289				
Qy	316	SMIGDWLVLSKTKYEEVGEIKAAHAEKAVNTAEFRTRRLSLVEIHKIQRAATISM	375				
Db	290	SMIGDWLVLSKTKYEEVGEIFRAHAETANTVAEFKTRRLSLVEIYDKQRATSV---	346				
Qy	376	ERRRGLDQRAHSLDMLSPKRSV	399				
Db	347	-KRKLSAELAGNHQELTFCMRTL	369				

Query Match 44.9%; Score 1238.5; DB 4; Length 370;

[illegible]

```

RESULT 5
US-09-432-470-2
; Sequence 2, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-2

```

Query Match	29.4%;	Score 812.5;	DB 4;	Length 393;
Best Local Similarity	53.8%;	Pred. NO. 1.6e-66;		
Matches 157;	Conservative 53;	Mismatches 77;	Indels 5;	Gaps 3
QY	67	MKWKTVVAFVWVWVLTGTVLFRALQPPESQKNTIALKKAFLRDHVCVSPQELST 126		
DB	1	MRSTTELLALLVLLVYLSGALVFRALQEPHEQQAQRELGEVREKFLRAHPCVSDQELGJ 60		
QY	127	LICHALDADNAGVSPIGNSNNSSH--WLGCSAFFAGTVTTITGYGNIAPSEGGKIFC 184		
DB	61	LKEVADALGGADPETHS:::SSSSSSANDLSAFFFSGTITITGYGNVALRDAGRLEFC 120		
QY	185	ILYAIGIFLFLAGIDQGLTTFGKSIARVKVPKQVQSOTKIRVISTITLFLIACG 244		
DB	121	IFPALYGIPLFGILLAGVDRGLSGSRHGIHIAIFLKHVPELVRVLSAMFLLLICG 180		
QY	245	IVFVTVPAVIFKYIEGWTALESIYVWVYLTATTVGSGDFVAGGNAGINREYWKPLVFWFI 304		

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Db      181 LLFVLITFTFFCYMEDSKLEAIFYVIVITLTTVCFGDYVAGADPRQD--SPAYQPLVWFWI 233
Oy      305 LVGLAYFAAVLSMITGDMRLVLSKTKBEVGSEIKAHAAEWKANVTAEPRETR 356
        :|::||::||::||::||::||::||::||::||::||::||::||::||:
Db      240 LLGLAYPASVLTTIGNMLRVVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 289

RESULT 6
US-09-432-470-4
; Sequence 4, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; CURRENT FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-4

```

Query Match	29.4%	Score 812.5	DB 4	Length 393
Best Local Similarity	53.8%	Pred. No. 1.6e-66		
Matches 157	Conservative 53	Mismatches 77	Indels 5	Gaps 3
QY	67	MKWKTTVAIFVVVVVLTGGLVFRALEQPPSESSQNTIALEKAEFLRDHVCVSPQELET	126	
DB	1	MRSSTTLTALLVLLVSLGALVFRALEQPEHQQAQRELGEVREKFLRAHPCVSDQELGL	60	
QY	127	LIQHALLDADNAGVSPIGNSSNNSSH-WDLGSAFFAGTAVLTTCYGNIASTEGGKIFC	184	
DB	61	LIKEVALGALGGADPETNSTSSNSHSAWDLGSAFFSGTIIITTCYGNVALRTDAGRLFC	120	
QY	185	ILYAIFGIFLPGFLLAGIGDOLGTFGKSIARVEKVPFKKQVSTQTKIRVISTILFLAGC	244	
DB	121	IFYALVGIFLPGIILLAGVDRGLGSSLRHGIGHIEAIFLKWHPPELVRLSAMFLPLIGC	180	
QY	245	IVFTYIETAVIKYTEGHTALESIFYVVVTLTTCVGGDFVAGNGAGINRYEWKPLVFWFI	304	
DB	191	LLFVLTPTTFVFCYMEDSKLEAIFYVIVTLTTCVGGDFVAGADPRQD-SPAYQPLVFWFI	239	
QY	305	LVGLAYTAAVLMSLDGDLVLVLSKTKTEEVGEIKAHAAEWKANVTAEPRTRR	356	
DB	240	LGLGLYASAVLTTCYGNLRLVYSRRTRAEKMGSLTQAAASWTCTGTA--RVTOR	289	

RESULT 7  
US-09-561-763-2  
; Sequence 2, Application US/09561763  
; Patent NO. 6664373  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J. et al.  
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MNT-074CP2  
; CURRENT APPLICATION NUMBER: US/09/561,763  
; CURRENT FILING DATE: 2000-04-29  
; PRIOR APPLICATION NUMBER: 09/431,367  
; PRIOR FILING DATE: 01-11-1999  
; PRIOR APPLICATION NUMBER: US 09/259,951  
; PRIOR FILING DATE: 01-03-1999  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 499

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-2

Query Match      17.5%; Score 483; DB 4; Length 499;
Best Local Similarity 25.8%; Pred. No. 6.2e-36;
Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;

QY 79 VVYIVTGLVFRALQPFSSQKNTALEKAEFURDHVCVSPQELTQHDAADNAG 138
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 12 IIFVLAIGAAIPEVLEEPHWKAEKNYYTQKHLHKEPPCLQEGDLKILEWSDAAGQ 71

QY 139 VSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNAPSTEGGKIFCILYAIFFGL 198
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 72 VAITGNQTFN--NWNWPNAMIFAATVTTTIGYGNVAPKTPAGRLFCVFGVPL--C 126

QY 199 LAGIGDQGTIFGKSIARVEKVFRRKQVSTQIRVISTILFILAGCIVFTTIPAVIFKYI 258
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFVWGLVHLVIPPVFMVT 185

QY 259 EGMTALESIFVVTUTTVGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVLSMI 318
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 186 EGMWYIEGLYSFITTSTIGDFVAGVNPSPANYHALYRYFVELWYILGLA----- 236

QY 319 GDMRLVLSKTKKEEVEIKAAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATIRSMERR 378
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 237 --WLSLF-----VNWKVS-----MFVEVHKAIK-----KRRRRR 263

QY 379 RGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNRLK-----GP 428
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 264 KESFESSPHSRKALQVKGSTASKDVNIFSLSKKEETVNDLIKQIGKKAMKTSGGGETGP 323

QY 429 -BQLNKHGOG-----ASEDNIINKFGSTSRLTKEKNKDLKKTLPED 468
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 324 GPGLGPOGGGLPALPPLVPLVVKVKNRVTLEEVSTQLRSKGHVSRSPDEEAVARAPED 383

QY 469 VOKIYKTFRNSLDDEKKEE-----TEKMCNSDSSSTAMLTDC 507
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 384 SSPAPEVFVN-QLDRISECEPWAQDYHPLIFQDASITFVNTAGLSDETSKSSLEDN 442

QY 508 I-----QCHAE-----LENGMIPTDTK 524
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 443 LAGEESPQOGAEAKAPLNMGEFPSSSE 469

RESULT 9
US-09-236-080-4
; Sequence 4, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-4

Query Match      16.2%; Score 447; DB 3; Length 107;
Best Local Similarity 77.6%; Pred. No. 1.2e-33;
Matches 83; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 144 NSSNNSHWDGSAFFAGTIVTTIGYGNAPSTEGGKIFCILYAIFFGLFGLAGIG 203
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 NSSNQVSHWDLGSSPFFAGTIVTTIGFNGNISPRTEGGKIFCIYALLGIPFLFLLAGVG 60

QY 204 DOLGTIFGKSIARVEKVFRRKQVSTQIRVISTILFILAGCIVFTTI 250
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 DQLGTIFGKSIARVEKVFRRKQVSTQIRVISTILFILAGCIVFTTI 107

RESULT 10
US-08-749-816-2
; Sequence 2, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel

```

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; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunski, Michel
; APPLICANT: Roney, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; TITLE OF INVENTION: OF DRUGS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-816-2

Query Match          14.6%; Score 403; DB 3; Length 336;
Best Local Similarity 33.2%; Pred. No. 8.2e-29;
Matches    95; Conservative      53; Mismatches 104; Indels   34; Gaps    9;

QY      76 FVVV-VVYLVTGLVPRALEQQFPSSCKNTIALEKAEFLRDHVCVSPQBLETLIQHALD 133
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      25 FLVLGYLLLVFGAVPSSVELPYEDLLRQLRKRLKRFLEEHECLSEQOQLGFLGRVLE 84
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY      134 ADNAGVSPIGNSNNSSHWDLGSAPFFAGTVITTTIGVGNLAPSTEGKGKIFCIYALFGIP 193
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      85 ASNVGVSVLNASGN-WNWFTSALFASIVLTSTGTGHVPLSDGSKAFCIYSVIGIP 143
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY      194 LFGFLLAGIDGDLGTIEFKGIARVEKYFRKKQV-----SOTKIRVI STL--PIA 242
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      144 FTLLFLTAV-----VQRITVHTVRPPVLVFHIRWGFSKVVAIVEALLGFVTV 192
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY      243 GCIVFTVIPAVIFXIE-GWTALESIFYVVVTLTVTGFGFVGAGNGAGINRYWKPLVW 301
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      193 SCFFFF--IPAAVFGVLEDNNFNLSFYFCFISLSTIGLDYVPGEGYNQKPRFLYKIGIT 250
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY      302 FWILVGLAYFAAVALSMIGDMRLVLSK----KTKEEVEGEIKAHAAE 342
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db      251 CYLLGLGLIAMLVLETCE-LHELKKPKRMFYVKDKDEQVHIIE 295
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||:

RESULT 11
US-09-144-914-2
; Sequence 2, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
```

Db 6 ARAAPEGRVRCVAVPG-----TVLLLLAYLAYLALGTGVFTLEGRAAQDSRSFQ 56  
 QY 107 LEKAEFLRDHVCVSPQLETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTIT 166  
 Db 57 RDKWELLQNTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115  
 QY 167 TIGYGNIAPTSEGGKIFCIIYAFIPIFGFLLAGIGDQIGTIFGKSIARVEKVRKKQV 226  
 Db 116 TIGYGNLSNTWAARLFCIFFALVGIPNLVVL-----NRLGHLMOQGVNHNASRLGGTQ 171  
 QY 227 SOTKIRVSTILFILAGCIVFTIPIAVFKYIEGTWTALESFYFVVVTLTTVGDFGVAGG 286  
 Db 172 DPKARWLAGSALLSGLLFLPLFPFLFSHMEGWSYTEGYFAPFIFLSTVGFDYVIGM 231  
 QY 287 NAGINREWYKPLVFWFVLVGLAYFAAVLSMI 318  
 Db 232 NPSQRYPLWYKNVSLWILFGMAWLALIKLI 263

## RESULT 13

US-09-431-367B-5

; Sequence 5, Application US/09431367B

; Patent No. 6670149

; GENERAL INFORMATION:

; APPLICANT: Curtis, Rory A.J.

; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

; FILE REFERENCE: MN-074CP

; CURRENT APPLICATION NUMBER: US/09/431,367B

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: 09/259,951

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-431-367B-5

## Query Match

; Sequence 5, Application US/09431367B

; Best Local Similarity 31.6%; Pred. No. 3.6e-28;

Matches 86; Conservative 58; Mismatches 114; Indels 14; Gaps 3;

QY 47 SRATVARMEGTSQGLQTVMKWKTVAIFVVVVVLTGVLVFALEQPPSSQKNTIA 106

Db 6 ARAAPEGRVRCVAVPG-----TVLLLLAYLAYLALGTGVFTLEGRAAQDSRSFQ 56

QY 107 LEKAEFLRDHVCVSPQLETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTIT 166

Db 57 RDKWELLQNTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115

QY 167 TIGYGNIAPTSEGGKIFCIIYAFIPIFGFLLAGIGDQIGTIFGKSIARVEKVRKKQV 226

Db 116 TIGYGNLSNTWAARLFCIFFALVGIPNLVVL-----NRLGHLMOQGVNHNASRLGGTQ 171

QY 227 SOTKIRVSTILFILAGCIVFTIPIAVFKYIEGTWTALESFYFVVVTLTTVGDFGVAGG 286

Db 172 DPKARWLAGSALLSGLLFLPLFPFLFSHMEGWSYTEGYFAPFIFLSTVGFDYVIGM 231

QY 287 NAGINREWYKPLVFWFVLVGLAYFAAVLSMI 318

Db 232 NPSQRYPLWYKNVSLWILFGMAWLALIKLI 263

## RESULT 14

US-09-362-842-14

; Sequence 14, Application US/09362842

; Patent No. 6511824

; GENERAL INFORMATION:

; APPLICANT: Buchman et al.

; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK

; CHANNELS AND METHODS OF USE

FILE REFERENCE: 7326-104  
 CURRENT APPLICATION NUMBER: US/09/362,842  
 CURRENT FILING DATE: 1999-07-28  
 PRIOR APPLICATION NUMBER: 09/270,767  
 PRIOR FILING DATE: 1999-03-17  
 NUMBER OF SEQ ID NOS: 70  
 SOFTWARE: Patent in Ver. 2.1  
 SEQ ID NO 14  
 LENGTH: 361  
 TYPE: PRT  
 ORGANISM: Leptinotarsa decemlineata  
 US-09-362-842-14

Query Match 13.1%; Score 361; DB 4; Length 361;  
 Best Local Similarity 29.1%; Pred. No. 6.9e-25;  
 Matches 86; Conservative 62; Mismatches 104; Indels 44; Gaps 7;

QY 41 PRLSISSRATVARMEGTSQGLQTVMKWKTVAIFVVVVVLTGVLVFALEQPPSS 100  
 Db 26 PKIVEGNRKIIIG-MEKTS-----PRFSLYLF-AYFMFLCSGAAVFSYFEAPEERA 74  
 QY 101 QKNTIALEKAEFLRDHVCVSPQLETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFF 160  
 Db 75 LRVLKGTAVQKELVSNPNVTADLEELIVEIVRANNGVSAIENAT-SEPNWSFGQSFF 133  
 QY 161 AGTVITTIYGNIAPTSEGGKIFCIIYAFIPIFGFLLAG-----IGDQ 205  
 Db 134 ASTVITTIYGHVTPLSNRNGLFCMFYAVVGIPLTLVLSALVERLLIPTVWLLQWLNSK 193  
 QY 206 LGTIFGKSIARVEKVRKKQVSTKIRVSTILFILAGCIVFTIPIAVFKYIE-GWTAL 264  
 Db 194 LGHLY-----QPLRIRIVHIAIIVLVLLVFFELLPAALPASLEPEWDYL 237  
 QY 265 ESIYFVVVTLTTVGDFGVAGGNAGINREWKYKPLVFWFVLVGLAYFAAVLSMIGD 320  
 Db 238 DSLYYCFISLTTIGLDYIPGDSAHQPYRPLKYKIMTTCVFLGITIMMLTLTVFYD 293

## RESULT 15

US-09-144-914-5

; Sequence 5, Application US/09144914

; Patent No. 6309855

; GENERAL INFORMATION:

; APPLICANT: Duprat, Fabrice

; APPLICANT: Lesage, Florian

; APPLICANT: Fink, Michel

; APPLICANT: Lazdunski, Michel

; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

; FILE REFERENCE: 989.6705CIP

; CURRENT APPLICATION NUMBER: US/09/144,914

; CURRENT FILING DATE: 1998-09-01

; EARLIER APPLICATION NUMBER: 08/749,816

; EARLIER FILING DATE: 1996-11-15

; EARLIER APPLICATION NUMBER: 60/095,234

; EARLIER FILING DATE: 1998-08-04

; EARLIER APPLICATION NUMBER: FR 96/01565

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 5

; LENGTH: 405

; TYPE: PRT

; ORGANISM: Murine

; FEATURE:

; OTHER INFORMATION: TASK

US-09-144-914-5

## Query Match 12.8%; Score 352.5; DB 4; Length 405;

Best Local Similarity 32.1%; Pred. No. 5.1e-24;

Matches 90; Conservative 53; Mismatches 110; Indels 27; Gaps 8;

QY 73 VAIFVVVVVLTGVLVFALEQPPSSQKNTIALEKAEFLRDHVCVSP---QELETLIQ 129

Db 6 LALIVCTFTYLLVGAAYFDALSEPEMIEQRLRQLE-LRARYNLSEGGYEELERVVL 64  
Qy 130 HALDADNAGVSPICNNSNNSSHWDLSAFFAGTVITTICYGNIAPSTEGGKIFCILIYAI 189  
Db 65 R-LKPHKAGV-----QWRPAGSFYFALTIVITTICYGHAAPSTDGKVFQCFYAL 112  
Qy 190 FGIPFGFLLAGIGDQLGTIFGKSIARVEKVKRQKVSQTKIRVISTILFILAGCIVFT 249  
Db 113 LGIPLTLIMFQSLGERINTFVRYLLHRAK---RGLGMRHAEVSMANNVLIGFVSCISTLC 169  
Qy 250 IPAVIPKVIIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINVREWKPLVWFILVGL 308  
Db 170 IGAAAFSYVERWTFQYIYCFITLTTIGFGDYVALQDQALOTQPYVAFSFFVILTGL 229  
Qy 309 AYFAAFLSMIGDMLRVLSKTKBEVGEIKAHAAEWNKANT 348  
Db 230 TVIGAFNLV--VLRFTMNAEDEKRD-----AEHRALLT 262

Search completed: June 29, 2004, 18:20:32  
Job time : 24 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 29, 2004, 18:19:28 ; Search time 50 Seconds  
(without alignments)  
3041.909 Million cell updates/sec

Title: US-09-892-360-2  
Perfect score: 2760  
Sequence: 1 MFPLYTDFLSLVAPAAAP.....IPTDKDREPENNLSLEDN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubaa/PTCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubaa/PTCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2760	100.0	538	12	US-09-892-360-2
2	2697	97.7	526	9	US-09-729-920-4
3	2697	97.7	543	9	US-09-729-920-2
4	2697	97.7	543	12	US-10-262-511-106
5	2697	97.7	543	12	US-09-852-386-73
6	2697	97.7	543	14	US-10-332-175-2
7	2657.5	96.3	724	12	US-10-332-447-10
8	2560.5	92.8	538	9	US-09-729-920-5
9	1248.5	45.2	411	9	US-09-828-746-6
10	1243	45.0	411	12	US-09-892-360-18
11	1242.5	45.0	411	9	US-09-828-746-2
12	1242.5	45.0	411	14	US-10-121-746-83
13	1238.5	44.9	370	9	US-09-939-484-8
14	1238.5	44.9	370	9	US-09-939-483-8
15	1218.5	44.1	426	8	US-08-816-011-45

16	825.5	29.9	1314	9	US-09-747-835A-29	Sequence 29, Appl
17	825.5	29.9	1314	12	US-10-312-312-29	Sequence 29, Appl
18	822.5	29.8	419	9	US-09-828-035-2	Sequence 2, Appl
19	822.5	29.8	419	14	US-10-345-680-44	Sequence 44, Appl
20	822.5	29.8	419	14	US-10-146-733-29	Sequence 29, Appl
21	822.5	29.8	419	15	US-10-352-684-8	Sequence 8, Appl
22	822.5	29.8	419	15	US-10-391-399-19	Sequence 19, Appl
23	812.5	29.4	392	9	US-09-747-835A-55	Sequence 55, Appl
24	812.5	29.4	392	12	US-10-312-312-55	Sequence 2, Appl
25	812.5	29.4	393	14	US-10-243-035-2	Sequence 19, Appl
26	790	28.6	398	12	US-09-892-360-19	Sequence 2599, Ap
27	610.5	22.1	421	12	US-10-276-774-2599	Sequence 2, Appl
28	512	18.6	294	12	US-10-451-892-2	Sequence 2, Appl
29	512	18.6	294	12	US-10-459-190-2	Sequence 9, Appl
30	512	18.6	294	12	US-10-459-190-9	Sequence 2, Appl
31	512	18.6	294	13	US-10-121-966-2	Sequence 2, Appl
32	512	18.6	309	15	US-10-080-334-172	Sequence 177, App
33	512	18.6	309	15	US-10-080-334-177	Sequence 11, Appl
34	511	18.5	239	12	US-10-459-190-11	Sequence 6, Appl
35	511	18.5	292	12	US-10-451-892-6	Sequence 10, Appl
36	511	18.5	292	12	US-10-451-892-10	Sequence 4, Appl
37	511	18.5	292	12	US-10-459-190-4	Sequence 2, Appl
38	483	17.5	499	9	US-09-735-169A-2	Sequence 2, Appl
39	483	17.5	499	9	US-09-735-171A-2	Sequence 2, Appl
40	483	17.5	499	12	US-10-701-013-2	Sequence 10, Appl
41	478	17.3	294	12	US-10-459-190-10	Sequence 13, Appl
42	455	16.5	239	12	US-10-459-190-13	Sequence 4, Appl
43	447	16.2	107	9	US-09-828-746-4	Sequence 2, Appl
44	403	14.6	336	9	US-09-939-484-2	Sequence 2, Appl
45	403	14.6	336	9	US-09-939-483-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-892-360-2  
; Sequence 2, Application US/09892360  
; Publication No. US20040101833A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LESAGE, FLORIAN  
; APPLICANT: ROMBY, GEORGES  
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE  
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND  
; TITLE OF INVENTION: RILUZOLE  
; FILE REFERENCE: 1256-R-00  
; CURRENT APPLICATION NUMBER: US/09/892,360  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 60/214,559  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 538  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-892-360-2

Query Match	100.0%;	Score	2760;	DB	12;	Length	538;
Best Local Similarity	100.0%;	Pred. No.	8.28-230;	Indels	0;	Gaps	0;
Matches	538;	Conservative	0;	Mismatches	0;		
QY	1	MFPLYTDFLSLVAPAAAPVCPKSA	100.0%;	Indels	0;	Gaps	0;
Db	1	MFPLYTDFLSLVAPAAAPVCPKSA	100.0%;	Indels	0;	Gaps	0;
QY	61	GGLOTVMKKTVAIVVVVVVLTGGLV	100.0%;	Indels	0;	Gaps	0;
Db	61	GGLOTVMKKTVAIVVVVVVLTGGLV	100.0%;	Indels	0;	Gaps	0;
QY	121	PQELFTLIHALDADNAGVSPIGNSN	100.0%;	Indels	0;	Gaps	0;
Db	121	PQELFTLIHALDADNAGVSPIGNSN	100.0%;	Indels	0;	Gaps	0;

Db 121 POELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGG 180  
QY 181 KIFCILYAIIFGLPFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFI 240  
Db 181 KIFCILYAIIFGLPFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFI 240  
QY 241 LAGCIVFTIPAVIPKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLV 300  
Db 241 LAGCIVFTIPAVIPKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLV 300  
QY 301 WFWILVGLAYFAVLVSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSV 360  
Db 301 WFWILVGLAYFAVLVSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSV 360  
QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
Db 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
QY 421 NNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYS 480  
Db 421 NNRLKGPOLNKHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYS 480  
QY 481 LDEEKEBETEHWKCNDSNSTAMLTDCCIQAHAELNGMIPTDTKDREPNNSLLEDNRN 538  
Db 481 LDEEKEBETEHWKCNDSNSTAMLTDCCIQAHAELNGMIPTDTKDREPNNSLLEDNRN 538

RESULT 2  
US-09-729-920-4  
; Sequence 4, Application US/09729920  
; Patent No. US20020103115A1  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000858  
; CURRENT APPLICATION NUMBER: US/09/729,920  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Human  
US-09-729-920-4

Query Match 97.7%; Score 2697; DB 9; Length 526;  
Best Local Similarity 100.0%; Pred. No. 2.2e-224;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSLISSRATVVARMEGTSGGGIQTVMKWT 72  
Db 1 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSLISSRATVVARMEGTSGGGIQTVMKWT 60  
QY 73 VAIFVFWVVLVTGGLVFRALQPPFESSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 132  
Db 61 VAIFVFWVVLVTGGLVFRALQPPFESSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 120  
QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAI 192  
Db 121 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAI 180  
QY 193 PLFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFILAGCIVFTIPA 252  
Db 181 PLFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFILAGCIVFTIPA 240  
QY 253 VIFKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 312  
Db 241 VIFKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 300  
QY 313 AVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAATI 372

Db 301 AVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAATI 360  
QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRPNRLKGPQOLN 432  
Db 361 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRPNRLKGPQOLN 420  
QY 433 KHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYSLDEEKEBETE 492  
Db 421 KHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYSLDEEKEBETE 480  
QY 493 MCNSDSSSTAMLTDCCIQAHAELNGMIPTDTKDREPNNSLLEDNRN 538  
Db 481 MCNSDSSSTAMLTDCCIQAHAELNGMIPTDTKDREPNNSLLEDNRN 526

RESULT 3  
US-09-729-920-2  
; Sequence 2, Application US/09729920  
; Patent No. US20020103115A1  
; GENERAL INFORMATION:  
; APPLICANT: GUEGLER, Karl et al  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; FILE REFERENCE: CL000858  
; CURRENT APPLICATION NUMBER: US/09/729,920  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Human  
US-09-729-920-2

Query Match 97.7%; Score 2697; DB 9; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.3e-224;  
Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSLISSRATVVARMEGTSGGGIQTVMKWT 72  
Db 18 VAVPAAAPVCPKSNATNGQPAPAPPTPTPLRSLISSRATVVARMEGTSGGGIQTVMKWT 77  
QY 73 VAIFVFWVVLVTGGLVFRALQPPFESSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 132  
Db 78 VAIFVFWVVLVTGGLVFRALQPPFESSQKNTIALEKAEFLRDHVCVSPQLETLIHAL 137  
QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAI 192  
Db 138 DADNAGVSPIGNSSNNSSHWDLGSAFFAGTIVTTIGYGNIAPISTEGGKIFCILYAI 197  
QY 193 PLFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFILAGCIVFTIPA 252  
Db 198 PLFGFLAGIGDGLTIFGKSIARVEKVFRRKQVSTQKIRVISTILFILAGCIVFTIPA 257  
QY 253 VIFKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 312  
Db 258 VIFKIEGTWTALESIFVFWVTLLTVGFGDFVAGNAGINREWKPLVFWILVGLAYFA 317  
QY 313 AVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAATI 372  
Db 318 AVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLSVIHDKLQRAATI 377  
QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRPNRLKGPQOLN 432  
Db 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRPNRLKGPQOLN 437  
QY 433 KHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYSLDEEKEBETE 492  
Db 438 KHGQASDNIINKFGSTSRLLTKRKNKDLKTLPEVQKIYKTFRYSLDEEKEBETE 497  
QY 493 MCNSDSSSTAMLTDCCIQAHAELNGMIPTDTKDREPNNSLLEDNRN 538

Db 498 MCNSDSSSTAMLTDCIQQAELNGMPTDTKDRPENNSLLEDRN 543

## RESULT 4

US-10-262-511-106

; Sequence 106, Application US/10262511

; Publication No. US20040038223A1

; GENERAL INFORMATION:

; APPLICANT: Smithson, Glenda

; APPLICANT: Millet, Isabelle

; APPLICANT: Feyman, John A.

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Ju, Jingfang

; APPLICANT: Li, Li

; APPLICANT: Guo, Xiaojia (Sasha)

; APPLICANT: Patturajan, Meera

; APPLICANT: Spyttek, Kimberly A.

; APPLICANT: Edinger, Shlomit R.

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel M.

; APPLICANT: Ort, Tatiana

; APPLICANT: Gorman, Linda

; APPLICANT: Zerhusen, Bryan D.

; APPLICANT: Anderson, David W.

; APPLICANT: Zhong, Mei

; APPLICANT: Catterton, Elina

; APPLICANT: Ji, Weizhen

; APPLICANT: Miller, Charles E.

; APPLICANT: Rastelli, Luca

; APPLICANT: Stone, David J.

; APPLICANT: Pena, Carol E. A.

; APPLICANT: Shenoy, Suresh G.

; APPLICANT: Shimkets, Richard A.

; APPLICANT: Rothenberg, Mark E.

; APPLICANT: Leach, Martin D.

; APPLICANT: Agee, Michele L.

; APPLICANT: Berghs, Constance

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

; FILE REFERENCE: 21402-462C

; CURRENT APPLICATION NUMBER: US/10/262,511

; CURRENT FILING DATE: 2003-05-28

; PRIOR APPLICATION NUMBER: 60/326,483

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: 60/373,815

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/327,917

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/381,642

; PRIOR FILING DATE: 2002-05-17

; PRIOR APPLICATION NUMBER: 60/328,029

; PRIOR FILING DATE: 2002-10-09

; PRIOR APPLICATION NUMBER: 60/381,038

; PRIOR FILING DATE: 2002-05-16

; PRIOR APPLICATION NUMBER: 60/328,056

; PRIOR FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 60/373,260

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: 60/373,826

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 60/327,435

; PRIOR FILING DATE: 2001-10-05

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 439

; SOFTWARE: CuroSeqList version 0.1

; SEQ ID NO 106

; LENGTH: 543

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-262-511-106

Query Match 97.7%; Score 2697; DB 12; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.3e-224;

Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCQPSKATNGQPAPAPPTPTPRLSISRATVVARMEGTSGGGLQTVNKKVT 72  
DB 18 VAVPAAAPVCQPSKATNGQPAPAPPTPTPRLSISRATVVARMEGTSGGGLQTVNKKVT 77  
QY 73 VAIFVVVVVYLVGTGLVFRALQEPPESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 132  
DB 78 VAIFVVVVVYLVGTGLVFRALQEPPESSQKNTIALEKAEFLRDHVCVSPQLETLIQHAL 137  
QY 133 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTYGYNTIAPSTEGGKIFCILYAFGI 192  
DB 138 DADNAGVSPIGNSSNNSSHWDLGSAFFPAGTVITTYGYNTIAPSTEGGKIFCILYAFGI 197  
QY 193 PLFGFLLAGIGDQGTIFGKSIARVEKVRKQVSOVKIRVISTILFILAGCIVFTIPA 252  
DB 198 PLFGFLLAGIGDQGTIFGKSIARVEKVRKQVSOVKIRVISTILFILAGCIVFTIPA 257  
QY 253 VIFKYIEGWTALSTYFVVVTLTTVVGDFGVAGNAGINREWKPLVWFVILVGLAYFA 312  
DB 258 VIFKYIEGWTALSTYFVVVTLTTVVGDFGVAGNAGINREWKPLVWFVILVGLAYFA 317  
QY 313 AVLSMIGDWLRVLSKTKKEEVEGEIKAAHAENKANVTAEFRETRRLSVIEHDKLQRAATI 372  
DB 318 AVLSMIGDWLRVLSKTKKEEVEGEIKAAHAENKANVTAEFRETRRLSVIEHDKLQRAATI 377  
QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 432  
DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPQLN 437  
QY 433 KHGQGAASEDNIINFGSTSLTKRKNKDLKKTLPEDVKIKYKTPNYSLBDEKKEETEK 492  
DB 438 KHGQGAASEDNIINFGSTSLTKRKNKDLKKTLPEDVKIKYKTPNYSLBDEKKEETEK 497  
QY 493 MCNSDSSSTAMLTDCIQQAELNGMPTDTKDRPENNSLLEDRN 538  
DB 498 MCNSDSSSTAMLTDCIQQAELNGMPTDTKDRPENNSLLEDRN 543

## RESULT 5

US-09-852-386-73

; Sequence 73, Application US/09852386

; Publication No. US20030064433A1

; GENERAL INFORMATION:

; APPLICANT: Roberts, Steven L.

; APPLICANT: Benjamin, Christopher

; APPLICANT: Karnovsky, Alla M.

; APPLICANT: Rubie, Cara L.

; TITLE OF INVENTION: Human Ion Channels

; FILE REFERENCE: 00133.US1

; CURRENT APPLICATION NUMBER: US/09/852,386

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: 60/203,305

; PRIOR FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: 60/207,092

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/206,526

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,033

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/207,093

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/216,893

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 60/237,873

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: 60/223,245

; PRIOR FILING DATE: 2000-08-04

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 73

; LENGTH: 543

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-852-386-73

Query Match 97.7%; Score 2697; DB 12; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-224;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATGPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 72  
 DB 18 VAVPAAAPVCPKSAATGPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 77  
 QY 73 VAIFVVVVVLTGGLVFRALQPPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132  
 DB 78 VAIFVVVVVLTGGLVFRALQPPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137  
 QY 133 DADNAGVSPIGNSSNNSSHDLSAPFFAGTIVTTIGYGNIAPTSTGGKIFCILYAFGI 192  
 DB 138 DADNAGVSPIGNSSNNSSHDLSAPFFAGTIVTTIGYGNIAPTSTGGKIFCILYAFGI 197  
 QY 193 PLFGFLLAGIGDQGLTIFGKSIARVEKVPFRKKQVSTQKIRVISTILFILAGCIVFVTIPA 252  
 DB 198 PLFGFLLAGIGDQGLTIFGKSIARVEKVPFRKKQVSTQKIRVISTILFILAGCIVFVTIPA 257  
 QY 253 VIFKYIEGWTALESIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVLVGLAYFA 312  
 DB 258 VIFKYIEGWTALESIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVLVGLAYFA 317  
 QY 313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLOAATI 372  
 DB 318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLOAATI 377  
 QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPEQLN 432  
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPEQLN 437  
 QY 433 KHGQGASEDNIINKFGSTSRITKRNKDLKKTLPEDVQKIYKTFRNSYSLDEKKEEETEK 492  
 DB 438 KHGQGASEDNIINKFGSTSRITKRNKDLKKTLPEDVQKIYKTFRNSYSLDEKKEEETEK 497  
 QY 493 MCNSDNSSTAMLTDCIQQAELENGMIPTDTKDRBPENNSLLEDNRN 538  
 DB 498 MCNSDNSSTAMLTDCIQQAELENGMIPTDTKDRBPENNSLLEDNRN 543

## RESULT 6

US-10-332-175-2  
 ; Sequence 2, Application US/10332175  
 ; Publication No. US20030176342A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
 ; TITLE OF INVENTION: No. US20030176342A1el potassium channel  
 ; FILE REFERENCE: Y0133PCT-666  
 ; CURRENT APPLICATION NUMBER: US/10/332,175  
 ; PRIOR FILING DATE: 2003-01-07  
 ; PRIOR APPLICATION NUMBER: JP 2000-396020  
 ; PRIOR FILING DATE: 2000-12-26  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SEQ ID NO 2  
 ; LENGTH: 543  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-332-175-2

Query Match 97.7%; Score 2697; DB 14; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-224;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATGPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 72  
 DB 18 VAVPAAAPVCPKSAATGPPAPPTPTPLRSSRATVVARMEGTSQGLQTVMKWKTIV 77  
 QY 73 VAIFVVVVVLTGGLVFRALQPPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132  
 DB 78 VAIFVVVVVLTGGLVFRALQPPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137

QY 133 DADNAGVSPIGNSSNNSSHDLSAPFFAGTIVTTIGYGNIAPTSTGGKIFCILYAFGI 192  
 DB 138 DADNAGVSPIGNSSNNSSHDLSAPFFAGTIVTTIGYGNIAPTSTGGKIFCILYAFGI 197  
 QY 193 PLFGFLLAGIGDQGLTIFGKSIARVEKVPFRKKQVSTQKIRVISTILFILAGCIVFVTIPA 252  
 DB 198 PLFGFLLAGIGDQGLTIFGKSIARVEKVPFRKKQVSTQKIRVISTILFILAGCIVFVTIPA 257  
 QY 253 VIFKYIEGWTALESIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVLVGLAYFA 312  
 DB 258 VIFKYIEGWTALESIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVLVGLAYFA 317  
 QY 313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLOAATI 372  
 DB 318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLOAATI 377  
 QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPEQLN 432  
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNRPNLRLKGPEQLN 437  
 QY 433 KHGQGASEDNIINKFGSTSRITKRNKDLKKTLPEDVQKIYKTFRNSYSLDEKKEEETEK 492  
 DB 438 KHGQGASEDNIINKFGSTSRITKRNKDLKKTLPEDVQKIYKTFRNSYSLDEKKEEETEK 497  
 QY 493 MCNSDNSSTAMLTDCIQQAELENGMIPTDTKDRBPENNSLLEDNRN 538  
 DB 498 MCNSDNSSTAMLTDCIQQAELENGMIPTDTKDRBPENNSLLEDNRN 543

## RESULT 7

US-10-332-447-10  
 ; Sequence 10, Application US/10332447  
 ; Publication No. US20040053258A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;  
 ; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;  
 ; APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;  
 ; APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;  
 ; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;  
 ; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameena R.;  
 ; APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;  
 ; APPLICANT: WALSH, Roderick T.; AU-YOUNG, Janice;  
 ; APPLICANT: LU, Yan; LU, Dzung Aina M.; AZIMZAI, Yalda;  
 ; APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Damiel B.;  
 ; APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;  
 ; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;  
 ; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.  
 ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS  
 ; FILE REFERENCE: PI-0149 USN  
 ; CURRENT APPLICATION NUMBER: US/10/332,447  
 ; PRIOR FILING DATE: 2003-01-07  
 ; PRIOR APPLICATION NUMBER: US 60/216,547  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/218,232  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/220,112  
 ; PRIOR FILING DATE: 2000-07-21  
 ; PRIOR APPLICATION NUMBER: US 60/221,839  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 10  
 ; LENGTH: 724  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20040053258A1 7472728CD1  
 US-10-332-447-10

Query Match

96.3%; Score 2657.5; DB 12; Length 724;

```
Best Local Similarity 98.7%; Pred. No. 9.5e-221;
Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTVMKWKT 72
Db 196 VAVPAAAPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTVMKWKT 255

QY 73 VAVPAAAPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTVMKWKT 132
Db 256 VAVPAAAPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTVMKWKT 315

QY 133 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTITTYGNIAPSTEGGKIFCILYAIFGI 192
Db 316 DADNAGVSPIGNSSNNSHWDLSGSAFFAGTITTYGNIAPSTEGGKIFCILYAIFGI 374

QY 193 PLFGFLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 252
Db 375 PLFGFLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 434

QY 253 VIFKYIEGWTALSIYFVVVTLTTVGDFVAVVFRGNAGINREWYKPLVFWILVGL 308
Db 435 VIFKYIEGWTALSIYFVVVTLTTVGDFVAVVFRGNAGINREWYKPLVFWILVGL 494

QY 309 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRETRRLSVIEHDKLQ 368
Db 495 AYFAAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRETRRLSVIEHDKLQ 554

QY 369 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASQESINNRPNRLKGP 428
Db 555 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASQESINNRPNRLKGP 614

QY 429 EQLNKHGQASDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEE 488
Db 615 EQLNKHGQASDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEE 674

QY 489 ETEKNCSDNSSTAMLTDCIOQHAELNGMIPTDTKDRPENNSLLEDRN 538
Db 675 ETEKNCSDNSSTAMLTDCIOQHAELNGMIPTDTKDRPENNSLLEDRN 724

RESULT 8
US-09-729-920-5
; Sequence 5, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-729-920-5

Query Match 92.8%; Score 2560.5; DB 9; Length 538;
Best Local Similarity 95.4%; Pred. No. 1.5e-212;
Matches 503; Conservative 9; Mismatches 8; Indels 7; Gaps 2;

QY 13 VAVPAAAPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVARMEGTSQGLQTVMKWKT 71
Db 18 VAVPAAAPVQPKSATNGH-----HFVPRLSISSRATVVARMEGASQGLQTVMKWKT 71

QY 72 VVAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIOHA 131
Db 72 VVAIFVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIOHA 131

QY 132 LDADNAGVSPIGNSSNNSHWDLSGSAFFAGTITTYGNIAPSTEGGKIFCILYAIFG 191
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132 LDADNAGVSPIGNSSNNSHWDLSGSAFFAGTITTYGNIAPSTEGGKIFCILYAIFG 191
QY 192 IPLFGFLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 251
Db 192 IPLFGFLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 251
QY 252 AVIFKYIEGWTALSIYFVVVTLTTVGDFVAVVFRGNAGINREWYKPLVFWILVGL 311
Db 252 AVIFKYIEGWTALSIYFVVVTLTTVGDFVAVVFRGNAGINREWYKPLVFWILVGL 311
QY 312 AAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRETRRLSVIEHDKLQ 371
Db 312 AAVLSMIGDMLRVLSKTKKEVGEIKAHAAEWKANVTAEFRETRRLSVIEHDKLQ 371
QY 372 IRSMERRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASQESINNRPNRLKGP 431
Db 372 IRSMERRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASQESINNRPNRLKGP 431
QY 432 NKHGGQASDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEE 491
Db 432 NKHGGQASDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKEE 491
QY 492 KMCNDSNDSSTAMLTDCIOQHAELNGMIPTDTKDRPENNSLLEDRN 538
Db 492 KMCNDSNDSSTAMLTDCIOQHAELNGMIPTDTKDRPENNSLLEDRN 538

RESULT 9
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

Query Match 45.2%; Score 1248.5; DB 9; Length 411;
Best Local Similarity 64.3%; Pred. No. 3.4e-99;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;

QY 17 ARAFPVQPKSATNGQPAPAPTPTPLRSLSSSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
Db 2 AAPDLDPKSA-----AQNSKPLSLSSKPTVLASVESDS----AINVMKWKIVSTI 50

QY 76 FVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIOHALDAD 135
Db 51 FLVVVLYLIIGAAVFRALQEPQEIISQRTTIVIQKOTFIAQHACVNSTELDELIQQVAAI 110

QY 136 NAGVSPIGNSSNNSHWDLSGSAFFAGTITTYGNIAPSTEGGKIFCILYAIFGIPLF 195
Db 111 NAGIIFLGNSSNVSHWDLSGSSFFAGTITTYGNIAPSTEGGKIFCIIVALLGIFLF 170

QY 196 GFLLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 255
Db 171 GFLLAGIGDQGITFGKSIARVEKVPKQVSOVKIRIVISTILFILAGCIVFVTIP 230
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QY 256 KYIEGWTALIESYFVVVTLTTVGFGDFVAGGNAGINREWKPLVWFWLVLGLAYFAAVL 315  
 Db 231 KHIEGWSALDAIFYFVVITLTTIGFGDYVAGG-SDIEYLDYFKPVVWFWLVLGLAYFAAVL 289  
 QY 316 SMIGDMLRVLSKTKKEEVEGEIKAAHAEKAWNTAFRETRRLSVEIHDKLOKORATIRSM 375  
 Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAEAWNTANVTAEFKETRRLSVEIYDKFORATSV--- 346  
 QY 376 ERRRLGDORAHSLDMLSPKRSV 399  
 Db 347 -RKLSAELAGNHNQELTPCMTL 369

## RESULT 10

US-09-892-360-18

; Sequence 18, Application US/09892360

; Publication No. US20040101833A1

; GENERAL INFORMATION:

; APPLICANT: LAZDUNSKI, MICHEL

; APPLICANT: LESAGE, FLORIAN

; APPLICANT: ROMEY, GEORGES

; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE

; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND

; FILE REFERENCE: RILUZOLE

; CURRENT APPLICATION NUMBER: US/09/892,360

; PRIOR FILING DATE: 2001-06-27

; PRIOR APPLICATION NUMBER: 60/214,559

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 18

; LENGTH: 411

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-892-360-18

## Query Match

Best Local Similarity 45.0%; Score 1243; DB 12; Length 411;

Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 17 AAAPVCQPKSATNGQPPAPPTPTPLRSISRATVVA-RMEGTSGGLQTVNMKWTVAI 75  
 Db 2 AAPDLLDPKSA-----AQNSKPLRSFSTKPTVLASRVESDT---TINVMKWTVTI 50

QY 76 FVVVVVLTGGLVFPALQPPESQKNTIALEKAEFLRDHVCVSPQLETLIOHALDAD 135  
 Db 51 FLVVVLYLIGATVPKALEQPHESQRTTIVIQKTFISQHSVCNSTELDELIOQIVAAI 110

QY 136 NAGVSPIGNSNNSHWDLGSAPFFAGTVITTIYGNIAPISTEGGKIFCILYALFIPLF 195  
 Db 111 NAGIIPLGNTSNQISHWDLGSFFAGTVITTIYGNISPRTEGGKIFCIYALLGIPLF 170

QY 196 GFLLAGIGDGLTIFGKSIARVEKVKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 255  
 Db 171 GFLLAGVGQGLTIFGKSIARVEKVKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 230

QY 256 KYIEGWTALIESYFVVVTLTTVGFGDFVAGGNAGINREWKPLVWFWLVLGLAYFAAVL 315  
 Db 231 KHIEGWSALDAIFYFVVITLTTIGFGDYVAGG-SDIEYLDYFKPVVWFWLVLGLAYFAAVL 289

QY 316 SMIGDMLRVLSKTKKEEVEGEIKAAHAEKAWNTAFRETRRLSVEIHDKLOKORATIR-- 373  
 Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAEAWNTANVTAEFKETRRLSVEIYDKFORATSKRX 349

QY 374 -SME-----RRRLGDORAHSLDMLSP 394  
 Db 350 LSAELAGNHNQELTPCMTLSVNLHTNWDVLP 383

## RESULT 11

US-09-828-746-2

; Sequence 2, Application US/09828746

; Patent No. US20020028485A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Helen Jane Meadows  
 ; APPLICANT: Conrad Gerald Chapman  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30031-D1  
 ; CURRENT APPLICATION NUMBER: US/09/828,746  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 09/236,080  
 ; PRIOR FILING DATE: 1999-01-25  
 ; PRIOR APPLICATION NUMBER: EP 98300570.3  
 ; PRIOR FILING DATE: 1998-01-27  
 ; PRIOR APPLICATION NUMBER: UK 9822135.1  
 ; PRIOR FILING DATE: 1998-10-09  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: Fast-Seq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 411  
 ; TYPE: PRT  
 ; ORGANISM: HOMO SAPIENS  
 ; US-09-828-746-2

Query Match 45.0%; Score 1242.5; DB 9; Length 411;

Best Local Similarity 63.5%; Pred. No. 11e-98;

Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVCQPKSATNGQPPAPPTPTPLRSISRATVVA-RMEGTSGGLQTVNMKWTVAI 75  
 Db 2 AAPDLLDPKSA-----AQNSKPLRSFSTKPTVLASRVESDT---TINVMKWTVTI 50

QY 76 FVVVVVLTGGLVFPALQPPESQKNTIALEKAEFLRDHVCVSPQLETLIOHALDAD 135  
 Db 51 FLVVVLYLIGATVPKALEQPHESQRTTIVIQKTFISQHSVCNSTELDELIOQIVAAI 110

QY 136 NAGVSPIGNSNNSHWDLGSAPFFAGTVITTIYGNIAPISTEGGKIFCILYALFIPLF 195  
 Db 111 NAGIIPLGNTSNQISHWDLGSFFAGTVITTIYGNISPRTEGGKIFCIYALLGIPLF 170

QY 196 GFLLAGIGDGLTIFGKSIARVEKVKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 255  
 Db 171 GFLLAGVGQGLTIFGKSIARVEKVKQVQKQVQKQVQKQVQKQVQKQVQKQVQKQV 230

QY 256 KYIEGWTALIESYFVVVTLTTVGFGDFVAGGNAGINREWKPLVWFWLVLGLAYFAAVL 315  
 Db 231 KHIEGWSALDAIFYFVVITLTTIGFGDYVAGG-SDIEYLDYFKPVVWFWLVLGLAYFAAVL 289

QY 316 SMIGDMLRVLSKTKKEEVEGEIKAAHAEKAWNTAFRETRRLSVEIHDKLOKORATIRSM 375  
 Db 290 SMIGDMLRVLSKTKKEEVEGEFRAHAEAWNTANVTAEFKETRRLSVEIYDKFORATSI--- 346

QY 376 ERRRLGDORAHSLDMLSPKRSV 399  
 Db 347 -RKLSAELAGNHNQELTPCMTL 369

## RESULT 12

US-10-121-746-83

; Sequence 83, Application US/10121746

; Publication No. US20030036648A1

; GENERAL INFORMATION:

; APPLICANT: Miller, Andrew P.

; APPLICANT: Curran, Mark Edward

; APPLICANT: Hu, Ping

; APPLICANT: Rutter, Marc

; APPLICANT: Wang, Jian-Wang

; TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels

; FILE REFERENCE: SEQ-15P

; CURRENT APPLICATION NUMBER: US/10/121,746

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: US/09/336,643A

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

```
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83

Query Match
45.0%; Score 1242.5; DB 14; Length 411;
Best Local Similarity 63.5%; Pred. No. 1.1e-98; Mismatches 66; Indels 17; Gaps 5;
Matches 244; Conservative 57;

QY 17 AAAPVCCPKSATNGQPPAPAPPTPTPLRSISSRATVVA-RMEGTSGGQTVNMKKTVAI 75
DB 2 AAPDLLDPKSA-----AQNKPRLSPSTKPTVLASRVESDT---TINVMKKTSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSQNTIALEKAEFLDHVCSVPOELETLIQHALDAD 135
DB 51 FLVVVLYLIIGATVFKALEQPEISQRTTIVIQKTFIQHSCVNSTELDELIQIIVAAI 110

QY 136 NAGVSPIGNSNSSNHWDLGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILYAFGIPLF 195
DB 111 NAGIIPLGNTSNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPLE 170

QY 196 GFLLAGIGDQLGTFGKSIARVEKVPKQVSTKIRVISTILFILAGCIVFTVPAVIF 255
DB 171 GFLLAGVGDQLGTFGKGIKAVEDTFIKWVNSQTKIRIISTITIFILFGCVLFAVPAIF 230

QY 256 KYIEGWTALESIIYVVVTLTTVGGDFVAGGNAGINREWKPLVWFILVGLAYFAAVL 315
DB 231 KHIEGWSALDAIYFVWTLTTIGFGDYVAGG-SDIEYLDYFKVPVWFILVGLAYFAAVL 289

QY 316 SMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANVTAEFRRRLSVSEIHDKIQRAATIRSM 375
DB 290 SMIGDMLRVLSKTKKEEVEGEFRAHAAEWANTVAEFKTRRLSVSEIYDKFORATSI--- 346

QY 376 ERRRLGDQRAHSLDMLSPKRSV 399
DB 347 -KRKLSAELAGNHQELTPCRTL 369

RESULT 13
US-09-939-484-8
; Sequence 8, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine

; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-484-8

Query Match
44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.2e-98;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;
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; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-484-8

Query Match
44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.2e-98;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAAPVCCPKSATNGQPPAPAPPTPTPLRSISSRATVVA-RMEGTSGGQTVNMKKTVAI 75
DB 2 AAPDLLDPKSA-----AQNKPRLSPSTKPTVLASRVESDS---AINVMKKTSTI 50

QY 76 FVVVVVYLVGTGLVFRALQEPFESSQNTIALEKAEFLDHVCSVPOELETLIQHALDAD 135
DB 51 FLVVVLYLIIGATVFKALEQPEISQRTTIVIQKTFIQHSCVNSTELDELIQIIVAAI 110

QY 136 NAGVSPIGNSNSSNHWDLGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILYAFGIPLF 195
DB 111 NAGIIPLGNTSNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPLE 170

QY 196 GFLLAGIGDQLGTFGKSIARVEKVPKQVSTKIRVISTILFILAGCIVFTVPAVIF 255
DB 171 GFLLAGVGDQLGTFGKGIKAVEDTFIKWVNSQTKIRIISTITIFILFGCVLFAVPAIF 230

QY 256 KYIEGWTALESIIYVVVTLTTVGGDFVAGGNAGINREWKPLVWFILVGLAYFAAVL 315
DB 231 KHIEGWSALDAIYFVWTLTTIGFGDYVAGG-SDIEYLDYFKVPVWFILVGLAYFAAVL 289

QY 316 SMIGDMLRVLSKTKKEEVEGEIKAHAAEWKANVTAEFRRRLSVSEIHDKIQRAATIRSM 375
DB 290 SMIGDMLRVLSKTKKEEVEGEFRAHAAEWANTVAEFKTRRLSVSEIYDKFORATSV--- 346

QY 376 ERRRLGDQRAHSLDMLSPKRS 398
DB 347 -KRKLSAELAGNHQELTPCVRT 368

RESULT 14
US-09-939-483-8
; Sequence 8, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-939-483-8

Query Match
44.9%; Score 1238.5; DB 9; Length 370;
Best Local Similarity 64.2%; Pred. No. 2.2e-98;
Matches 246; Conservative 52; Mismatches 68; Indels 17; Gaps 5;
```

QY 17 AAPVCPKPSATNGOPAPAPPTPTPLSLSSRATVVA-RMEGTSGGLQTVMKKTVAI 75  
 Db 2 AAPDLLDPKSA-----AQNSKPLSLSPSTKPTVLASRVESDT---AINVMKKTVSTI 50  
 QY 76 FVVVVYLVGTGLVFRALPQPESSQKNTIALEKAEFLRDHVCVSPQSELETLIQHALLDAD 135  
 Db 51 FLVWVLYLTIGAAVFKALEPQPEISORTTIVIQKQTFIAQHACVNSTELDELIQIIVAAI 110  
 QY 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIIGYCNIAPTSTEGKIFCILYAIFGIPLF 195  
 Db 111 NAGIIPLGNSNQVSHWDLGSSFFAGTVITTIIGYCNISPRTEGKIFCIITVALLGIPLE 170  
 QY 196 GFLLAGIGDQGTIFGKSIARVEKVRKQVSTQKIRVISTILFILAGCIVFVTPAVIF 255  
 Db 171 GFLLAGVGDQGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILGCVLFVALPAVIF 230  
 QY 256 KYIEGWTALIESYFVVVTLTTVGFDFVAGNAGINREWKPLVWFILVGLAYFAAVL 315  
 Db 231 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDIFYKPVVWFILVGLAYFAAVL 289  
 QY 316 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANYTAETRETRRLSVEIHDKLQRAATIRSM 375  
 Db 290 SMIGDMLRVLSKKTKEEVEGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSV--- 346  
 QY 376 ERRRLGLDQRAHSLDMLSPKESV 398  
 Db 347 -KRKLSAELAGNHQELTFCRATL 368

## RESULT 15

US-08-816-011-45  
 ; Sequence 45, Application US/08816011  
 ; Publication No. US20030165806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Price, Laura A.  
 ; APPLICANT: Pausch, Mark H.  
 ; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences  
 ; TITLE OF INVENTION: Encoding Them, and Methods of Using Same  
 ; NUMBER OF SEQUENCES: 56  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: American Home Products Corporation  
 ; STREET: One Campus Drive  
 ; CITY: Parsippany  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07054  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/816,011  
 ; FILING DATE: 11-MAR-1997  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Matthews, Gale F.  
 ; REGISTRATION NUMBER: 32,269  
 ; REFERENCE/DOCKET NUMBER: 32,421-C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-683-2134  
 ; TELEFAX: 201-683-4117  
 ; INFORMATION FOR SEQ ID NO: 45:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 426 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear

US-08-816-011-45

Query Match 44.1%; Score 1218.5; DB 8; Length 426;  
 Best Local Similarity 62.8%; Pred. No. 1.4e-96;  
 Matches 241; Conservative 58; Mismatches 68; Indels 17; Gaps 5;

QY 17 AAPVCPKPSATNGOPAPAPPTPTPLSLSSRATVVA-RMEGTSGGLQTVMKKTVAI 75  
 Db 17 AAPDLLDPKSA-----AQNSKPLSLSPSTKPTVLASRVESDT---TINVVMKKTVSTI 65  
 QY 76 FVVVVYLVGTGLVFRALPQPESSQKNTIALEKAEFLRDHVCVSPQSELETLIQHALLDAD 135  
 Db 66 FLVWVLYLTIGAAVFKALEPQPEISORTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAI 125  
 QY 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITTIIGYCNIAPTSTEGKIFCILYAIFGIPLF 195  
 Db 126 NAGIIPLGNSNQISHWDLGSSFFAGTVITTIIGYCNISPRTEGKIFCIITVALLGIPLE 185  
 QY 196 GFLLAGIGDQGTIFGKSIARVEKVRKQVSTQKIRVISTILFILAGCIVFVTPAVIF 255  
 Db 186 GFLLAGVGDQGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILGCVLFVALPAVIF 245  
 QY 256 KYIEGWTALIESYFVVVTLTTVGFDFVAGNAGINREWKPLVWFILVGLAYFAAVL 315  
 Db 246 KHIEGWSALDAIFYVVTITTTIGFGDYVAGG-SDIEYLDIFYKPVVWFILVGLAYFAAVL 304  
 QY 316 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANYTAETRETRRLSVEIHDKLQRAATIRSM 375  
 Db 305 SMIGRLVRVISKKTKEEVEGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSI--- 361  
 QY 376 ERRRLGLDQRAHSLDMLSPKESV 399  
 Db 362 -KRKLSAELAGNHQELTFCRATL 384

Search completed: June 29, 2004, 18:25:28

Job time : 51 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2004, 18:15:42 ; Search time 21 Seconds  
(without alignments)  
2464.335 Million cell updates/sec

Title: US-09-892-360-2

Perfect score: 2760

Sequence: 1 MFPLYTDFPLSLVAPAAAP.....IPTDTKDRPENNSLLSDRN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	403	14.6	336	2 S65566	inward rectifier p
2	329	11.9	330	2 JC7703	TASK-5 protein - h
3	326	11.8	1001	2 T13807	potassium channel
4	315.5	11.4	329	2 T43509	probable potassium
5	307	11.1	336	2 T32347	outward rectifier
6	300.5	10.9	364	2 T43361	probable potassium
7	298.5	10.8	393	2 T25392	hypothetical prote
8	298.5	10.8	1910	2 H88124	protein T12C9.3 [1
9	290.5	10.5	334	2 T19860	hypothetical prote
10	282.5	10.2	392	2 T45032	hypothetical prote
11	268.5	9.7	522	2 T24265	hypothetical prote
12	265.5	9.6	528	2 T21834	hypothetical prote
13	264.5	9.6	444	2 T26223	hypothetical prote
14	264	9.6	551	2 T16426	hypothetical prote
15	264	9.6	555	2 T43357	potassium channel
16	262.5	9.5	443	2 T21538	hypothetical prote
17	260	9.4	461	2 T43394	potassium channel
18	258.5	9.4	513	2 T28933	hypothetical prote
19	255	9.2	452	2 T21118	hypothetical prote
20	252.5	9.1	586	2 T21693	hypothetical prote
21	248	9.0	325	2 T15594	hypothetical prote
22	247	8.9	427	2 T27691	hypothetical prote
23	245	8.9	1136	2 T26953	hypothetical prote
24	244	8.8	504	2 T22269	hypothetical prote
25	233.5	8.5	484	2 T43529	probable potassium
26	233.5	8.5	519	2 T16829	hypothetical prote
27	233.5	8.5	1539	2 T30037	hypothetical prote
28	229.5	8.3	383	2 T23182	hypothetical prote
29	227.5	8.2	307	2 H89074	protein twk-24 [lm

30	224.5	8.1	524	2 T23907	hypothetical prote
31	224.5	8.1	769	2 T27550	hypothetical prote
32	221.5	8.0	643	2 T26616	hypothetical prote
33	218	7.9	335	2 S44635	f22b7.7 protein -
34	217.5	7.9	691	2 S46585	outward-rectifier
35	216.5	7.8	576	2 T43363	potassium channel
36	213.5	7.7	660	2 T21551	hypothetical prote
37	213	7.7	569	2 T43531	probable potassium
38	210.5	7.6	544	2 T43364	potassium channel
39	208.5	7.6	485	2 T4201	hypothetical prote
40	207.5	7.5	700	2 T27364	hypothetical prote
41	204.5	7.4	550	2 T22557	hypothetical prote
42	203.5	7.4	539	2 T23700	hypothetical prote
43	202	7.3	681	2 T19429	hypothetical prote
44	198	7.2	631	2 T26232	hypothetical prote
45	189.5	6.9	475	2 T27725	hypothetical prote

ALIGNMENTS

RESULT 1

S65566 inward rectifier potassium channel TWIK-1 - human

C:Species: Homo sapiens (man)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 05-Nov-1999

C:Accession: S65566

R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, J.

EMBO J. 15, 1004-1011, 1996

A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel st

A:Reference number: S65566; MUID:96183184; PMID:8605869

A:Accession: S65566

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-336 <LES>

A:Cross-references: EMBL:U33632; NID:gi086490; PIDN:AAB01688.1; PID:gi086491

Query Match 14.6%; Score 403; DB 2; Length 336;

Best Local Similarity 33.2%; Pred. No. 1.1e-20;

Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;

QY	76	FVVV--VVYVTGLVFRALQEPFSSOKNTALIEKAEFLRDHVCVSPQELTLIQHAI	133
DB	25	FLVGLVLYLVGAVVFSVVELPYEDLLRQELRKLKRFLEHECLSQQLQFGRVLE	84
QY	134	ADNAGVSPIGNSSNNSHWDLGSAFFAGTVITITGYNIAFSTEGGKIFCLYAFGIP	193
DB	85	ASNYGVSVLSNASGN--WNWDFTSALFFASTVLTSTGYGHTVPLSDGKAFCTIYSVIGIP	143
QY	194	LFGLIAGIGDGLGTIFGKSIARVEKVRKKQV-----SQTKIRVISITL--FILA	242
DB	144	FTLLFLTAV-----VORITVHTRPVLYFHIRWGFSKQVVAIVRAVLGFTV	192
QY	243	GCIVFTVTPAVIFKVIKIE--GWTALSIYFVWVTLTTVGFDFVAGNAGINREWKPLVW	301
DB	193	SCFFF--IPAAVFSVLEDDNWFLESFYCFISLTIGLDVYVPGBYNQKPRELYKIGIT	250
QY	302	FMILVGLYFAAFLVMSIGDWLVLSK-----XTRKEVCEIKAAHAE	342
DB	251	CYLLGLIAMLVLETFCE--LHELKXFRMFVYVKDDEQVHIIE	295

RESULT 2

JC7703

TASK-5 protein - human

C:Species: Homo sapiens (man)

C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

C:Accession: JC7703

R:Kim, D.; Gnatenko, C.

Biochem. Biophys. Res. Commun. 284, 923-930, 2001

A:Title: TASK-5, a new member of the tandem-pore K+ channel family.

A:Reference number: JC7703; MUID:21303050; PMID:11409881

A:Accession: JC7703



C; Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C; Accession: T32347  
R; Murray, J.; Wohldmann, P.; O'Neal, D.  
submitted to the EMBL Data Library, September 1997  
A; Description: The sequence of C. elegans cosmid F34D6.  
A; Reference number: Z21153  
A; Accession: T32347  
A; Status: preliminary; translated from GB/EMBL/DBJ  
A; Molecule type: DNA  
A; Residues: 1-336 <MUR>  
A; Cross-references: PIDN: AAC71151.1; GSPDB: GN000020; CESP: F34D6.3  
A; Experimental source: strain Bristol N2; clone F34D6  
C; Genetics:  
A; Gene: twk-23; CESP: F34D6.3  
A; Map position: 2  
A; Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 295/3

Query Match	11.1%;	Score 307;	DB 2;	Length 336;
Best Local Similarity	30.3%;	Pred. No. 5.5e-14;		
Matches	84;	Conservative 50;	Mismatches 101;	Indels 42; Gaps 9;
Qy	73	VAIPVVVVVIVTGGVFRALQEPFESSQKNTIALERAEFLRDVCVSPQOELETLIGHAL	132	
Db	9	LSLIVCTLTLLVGAADVDALETENEILQVRGLG-	55	
Qy	133	-----DADNAG-----VSPIGNSSNNSSHWDLGSAFFAGTAVTTTIGVGNATPSTEGG	180	
Db	56	KTKYNNMNDYVEILEATIVKSVPHKA--GQWKESGAFYFATVTTTIGYGHSTPMTDAG	113	
Qy	181	KIFCILYAIFGPIPLFGFLLAGIGDQGLTIFGKSJARVEKVKRQVQSQTIRVISTILFI	240	
Db	114	KVFCMLYALAGIPLGLIMFOSIGERMNTFAAKLRFIRRAAGKQPI-----VTSSDLII	167	
Qy	241	L-----ACIVFVTIPAVIEKYIEGWTALESIFYVVVTLTITVGFDDFVAGGNAG--INVRE	295	
Db	168	FTCWGGLLIIFG--GAPMFSSYENWTVFDVYYCFVTILTIIGFGDYVALQKRGSLQVPE	225	
Qy	296	YKPLVFWTIVLGLYAFAAVLSMIGDWLRVLSKTKKEE	332	
Db	226	YVFPESLVFIIFGLGVIAAAMNLL--VLRFTMTNTEDE	260	

```

RESULT 6
T43361
probable potassium channel chain n2P20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C:Accession: T43361
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-364 <WAN>
A:Cross-references: EMBL:AF083646; PIDN:AAC32857.1

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	Query Match	10.9%	Score 300.5;	DB 2;	Length 364;
	Best Local Similarity	26.8%	Pred. No. 1.8e-13;		
	Matches 106;	Conservative 78;	Mismatches 124;	Indels 87;	Gaps 19;
Qy	70 KTVVAIFVW--VVYLTGGIVAFRALEQFPFSSOKNTIALEKAFRLRDHV----	CVSPOE 123			
Db	7 KSRALLILILGTFYLLFGAVVPDKLE-----SKDTWVRDEIRITDRLKHKNFSERD 61				
Qy	124 LETLIQHALDADNAGVSPIGNSSNNSSHHWDIGSAFFAGTVITTTIGYGNIAPTSGGGKIF 183				
Db	62 L-----HLFEA--TAIKSI PQQA--GYWQFAGAFYFATVITTVGYCHSAPSTNAGKLF 112				
Qy	184 CILYAIATGIPLPGFELLAGIGDQGLTIFGKSTARVEKVKPK-----KQVSQTKIRVTS-T 236				
Db	113 CMIFALGVPMGLLMFOSIGIRVENATFYATSLHKFRSDLSHUQGFQCLQEVTFHLLMVSFLT 172				

```

237 QY ILP--ILAGCIVFTIPAVIFKYIEGHTALESIFVWVTLTTVGFQDGFVAGGNAGINYPE 294
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
173 Db IGFVWIVSGTYNFT-----IEKWSIFDAYIFCMITFTSTIGFGDLVP--LQQVNALQ 222
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
295 QY WYKPLWF-----WILVGLAYFAAIVLSIGMDLRLVSKKTKEEVGEIKAHAAAEKAVVTAE 350
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
223 Db -DQPLVVVATIMFILLGLAVFSACVNL-----VLGFVMSNADE-----VTAA 264
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
351 QY -----TPRRLSVEIHDKLRQAATIRSMERRRLGLDORAHSLDMLS----- 393
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
265 Db QREPSAIVLERFTNSLVDSQIFNIQKSTVGVLP-----GRFRMYSVIPNSTADVHLR 320
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
394 QY --PEKRSVFAALDTGRFKASSQE---SINRRPNNL 423
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
321 Db RSTRRSIQDTVCCGCFKPRPRHRFSLTRRPTNI 355
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 7
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25392

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K/Lloyd, C.  
submitted to the EMBL Data Library, March 1997  
A;Reference number: Z20027  
A;Accession: T25392  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-393 <WILL>  
A;Cross-references: EMBL:Z292813; PIDN:CAB07286.1; CESP:T28A8.1  
A;Experimental source: Clone T28A8  
C;Genetics:  
A;Gene: CESP:T28A8.1  
A;Map position: 3  
A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match	10.8%	Score 298.5;	DB 2;	Length 393;
Best Local Similarity	27.1%	Pred. No. 2.7e-13;		
Matches	85;	Conservative	50;	Mismatches 94;
				Indels 85;
				Gaps 11

Qy	69	WKTIV-----VAIFVVVVLVTGGLVFRALEOPPESSOKNTIALEKAEFLRDHVCVSP	121
Dd	4	WKTYARILAHVSLTVLSVYVGGAFLFYOLEP-----NEVEVRARNIERFNI-----	53
Qy	122	QELETLIQHALDADNAGVSP-----IG-----NSSNS	149
Dd	54	-HKRQMEHLWEEMRESSIGQHWEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGED	112
Qy	150	SHWDLGSAFFFRAGTWTITGVGNATAPSTEGKIFCILYAIFGIPLFGFLAAGIDOLGTI	209
Dd	113	YNWYMTALFTTTTLTGITGNTLPVPTGRKLCLILYALFGVPL-----ILITVAD-IGKF	168
Qy	210	FQKSIAERVEKVERK--KVQSOTKIRVIST-----ILFIAGCT	245
Dd	169	LSENIVOLTYRWYRLREKCSQKYSVISSDKDNKEGDLNDHLENYSISIPILVAIL	228
Qy	246	VFTTPPAVIFKYEIGWTALBESLYFWVTLTGVFGDFVAGGNAGINRYEWKPLVWFIL	305
Dd	229	SYITGANVLSNWGEWDFSGFYFSFTMTTVGGDIVP-----LKREYY-IDLCYII	281
Qy	306	VGLAYFAAVLSMIG	319
Dd	282	IGLSITTMCIDLVG	295

```

RESULT 8
H88124
protein_T12C9.3 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C/Accession: H88124

```

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: AF5000; MUID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: H88124

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1910 <STO>

A:Cross-references: GB:chr\_II; PIDN:ACT1141.1; PID:gl086770; GSPDB:GN00020; CESP:T12C9.3

A:Note: proline-rich

C:Genetics:

A:Gene: T12C9.3

A:Map position: 2

Query Match 10.8%; Score 298.5; DB 2; Length 1910;  
Best Local Similarity 21.2%; Pred. No. 2.2e-12;  
Matches 121; Conservative 90; Mismatches 197; Indels 163; Gaps 22;

QY 10 LSLVAVPAAAPVCPKSAATNGPPAP-APTP---TPRLSISRRATVVARMEGTSGGGLQT 65

DB 134 LSFSPATRAKLSQV---HPPIPHPTPPQSRFRSIFPGLESARPDDETTITLQN 190

QY 66 VNKWTV---VAIFVVVVVLTGGLVFRALQPFESSQK---NTIALEKA----- 110

DB 191 IRKYAKLALPHIVLVVCVCIATIGAWIFTLESPNEDRLKXETGRKTAEMRSLYKIN 250

QY 111 -----EFLRDHVCVPOEL-----ETLQHA-----LDADNAGVSPIGN 144

DB 251 NNEKEVWEDTEKELMLYSEKLYKAFKQYRYSDVRTIGEGRSSVEEADTG---GD 306

QY 145 SNNSNH-----WDGSAFFPAGTVITTYGNIAPSTEGGKIFCILYAI 190

DB 307 SERKRRHRGNKRGSGSEKMTWTSALLFAATTMTATIGYGNIVPVLGLACVLPALF 366

QY 191 GIPLFGPILLAGIDGLG-TIF-----CKSTARVEKVKRK----- 223

DB 367 CAPTAITIGDLGKFLSCTILWKYMKRGASLDASAKRFRGLSDSDDLESASKNQD 426

QY 224 -----KQVSTQKIRVISTILFILAGCIVFVTIPAVIFKYIEGTALSIYFVVVTLT 275

DB 427 SSILDMMDDEIDKSEVPVLMVFTIIL-----LYIAFGILFSLSDWSYMDAFYYSFISLT 482

QY 276 TVGFGDFVAGGNAGINREWKPLWFILVGLAYFAAVLSMIG----- 319

DB 483 TIGFGDIVPENHD-----YIAIMLIYLVGLSVTTWCIDLAGIQYIKIHYGKRFQ 535

QY 320 -DWLRVLSKTK-----EEVGEIKAHAAEWKANVTAEFRETERRLSVEIHDKLQR 368

DB 536 TDLQLYKKKMLERLAWGGEILRYKHAVE-----KFEREQEQQLQKMEEDPP 598

QY 369 AATRSMERRLGLDQRAHSL-----DMLSEKRSV---FALDTRGRFASQES 415

DB 589 SIEGKGFNSMWRIDDSUSALQRLFYDTYDEDLFSPTIHSVRFSQVMSHSSARSQS 648

QY 416 I---NNRPNLRLKGPEOLNKHGQASDNI 443

DB 649 CRFQENRGASWDESGP-SLSEHCSLSTPSV 678

# RESULT 9

T19860

hypothetical protein C40C9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T19860

R:Hembry, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z19188

A:Accession: T19860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <WIL>

A:Cross-references: EMBL:270266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.1

A:Map position: X

A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 10.5%; Score 290.5; DB 2; Length 334;

Best Local Similarity 28.6%; Pred. No. 7.8e-13;

Matches 89; Conservative 67; Mismatches 94; Indels 61; Gaps 15;

QY 70 KTVVAIFVVV--VYLVTVGGLVFRALQPFESSQKNTIALEKAEFLRDHV---CVSQOE 123

DB 7 KSAALLLILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLKHKYNSERD 61

QY 124 LETLIQHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTVITTYGNIAPSTEGGKIF 183

DB 62 L-----HLFEA---IAKSIPOQA--GYQMFAGAFYFATVITTYGHSASTNAGKLF 112

QY 184 CILYAIFFGIPLFGLIAGIGDQIGTFGKSIARVEKVKRK-----KQVSTQKIRVIS-T 236

DB 113 CMIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQOQFTCLQEVTPTHLLMVSIL 172

QY 237 ILF--ILAGCIVFVTIPAVIFKYIEGTALSIYFVVVTLTVGDFVAGGNAGINRE 294

DB 173 IGFVIVSVSTYMFHT-----IEKWSIFDAYFCMIFSTIGFGDLVP--LQOVNALQ 222

QY 295 WYKPLVWF---WILVGLAYFAAVLSMIGMDLRLSKTKKEVGEIKAHAAEWKANVTAE 350

DB 223 -DQPLVVFATIMFILLGLAVFSCVNLL-----VLGFWSNADN-----VTAA 264

QY 351 FRETERRLSVE 361

DB 265 QREPPSAIVLE 275

# RESULT 10

T45032

hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T45032

R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, C.

razer, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johnston

B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.

Nature 368, 32-38, 1994

A:Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, E.; St

tock, L.; Wilkinson-Sproat, J.; Wohldman, P.

A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.

A:Reference number: S43531; MUID:94150718; PMID:7906398

A:Accession: T45032

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-392 <WIL>

A:Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446

A:Experimental source: clone Y39B6B

C:Genetics:

A:Map position: 3

A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3

A:Note: Y39B6B.f

Query Match 10.2%; Score 282.5; DB 2; Length 392;

Best Local Similarity 31.7%; Pred. No. 3.5e-12;

Matches 77; Conservative 46; Mismatches 97; Indels 23; Gaps 8;

QY 90 FRALQPFESSQKNTIALEKAEFLRDHVC---VSPQETLIQHALDADNAGVSPIGNSS 146

DB 118 FSRIEYPLEKIEREAY-LDYQNWQDRLIQDIDSEIDKLF---LNTREALNIWMDR 173

QY 147 NNSN--HWDLGSAFFAGTVITTYGNIAPSTEGGKIFCILYAIFFGLIAGIGD 204

DB 174 NLTSDPNWTFGQAFPAAGTILSTVGYGRVSPTEYKGLFTILYCVIGIPLTLALISAIVA 233

[illegible]

Query Match	9.6%;	Score 265.5;	DB 2;	Length 528;
Best Local Similarity	22.2%;	Pred. No. 8e-11;		
Matches 122;	Conservative 86;	Mismatches 163;	Indels 179;	Gaps 26
Qy	79	VVVYLVTVGLVFRAL	-----QPFE-----SQKNTIALEKA	110
Db	25	VVLYITGAIVFQMLEGHLNDFDNFKKHFGKQVVDKFFETIFRRWSKGAN	---FKKS	81
Qy	111	EFLRDHVCVSPQ	-----ELETLI-----QHALDADNAGVSP	142
Db	82	ALKKHMAKIEQNAKDYDKLWSVAKSDRDKYKNVEDLKSXVEDIVDDENDYVDVFFYA	141	
Qy	143	-----GNSNNSSHWDLSGAPFFAGTVITIGYGNIAPISTEGGKIICILYAIPIGLPFG	197	
Db	142	HRAVRHGVDSDPTWDFANSVFTTMLTIGIGYVAPSTFGGLRFGVYICLIGIPLTIV	201	
Qy	198	LLAGIGDGLG-TIF	-----GKSIARVEKVFRRKKVQSQ-----TKIR	232
Db	202	TVANVAKFLSEITIFELHYELNKCLEWKRK	-RKGEVEADPLQPMFGDDENBEILDRVR	259
Qy	233	VIS-----TILFLIACIIVTIPAVIPKYTEGNTALESYFVVVVTTITTVGCGDF-VAGGN	287	
Db	260	LVRFPPLTVPFV	---FVYGGIAAWVRVYETWTYVESLYFISITITVGFGDIRDSPGN	316
Qy	288	AGINREWKPIVWF	---WILVGLAYFAAFLSMITGM-----LRLVSKTKTEE-----VGE	335
Db	317	-----IWTLAFVVVGVLITITMCMDDVVGRWYLMKEIHYLGRKLSKSNPFYLLRE	364	
Qy	336	IKAHAAEWKANTAFETRRRLSV	-----EIHDKLQRAATIRSMERREL	380
Db	365	AKAR	-----RRRAWASLLAQLAKGMIFAKHDYNELARKSKRKKKEKR	408
Qy	381	GLDORASHLDMLSPKRSVFAALDTGRFKASSQESINNRPNNLRLKGPBOLNKHGGQASE	440	
Db	409	-----GSHVL-----PNEKTFMARLPD	-PFSDCQWSTSAYSVRLAWAPF-----SP	451
Qy	441	D-----NIINKEGTSRLTKKKNKDLKTLPEDYQKLYKTFRNSYLDEEKKETEKC	-494	
Db	452	DDPLTINIRYRLNATVFKDQGRSPLSEALFIKTDKI	--EFHKHCYGHSTKIDVMDSICE	509
Qy	495	NSDNSSTAML	504	
Db	510	KEDNETTALL	519	

RESULT 13  
T26229  
hypothetical protein W06D12.2 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T26229

A,Map position: X  
A;Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

Query Match 9.6%; Score 264; DB 2; Length 551;  
Best Local Similarity 20.3%; Pred. No. 1.1e-10;  
Matches 108; Conservative 94; Mismatches 205; Indels 124; Gaps 16;

QY 74 AIFVWVVLVTGVLVFRALPQPESSQKNTIALEKAEFLRDHVCVSPQBLETL----- 127  
DB 24 SLLMLVLLYSFLGGFIDRIETNAHEMK-----RNERINRTACVS-QILHSIHWSHN 76  
QY 128 ----IQHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTVITTIYGNIAPESTGGKIF 183  
DB 77 QTHKVOVAEDIAC----FEPEKDERSEWNVFTATLYGFGIVTLTGYNRIAPITYTGRMF 132  
QY 184 CILYAIFGIPLFGFLAGIGDQGTIFGKSIAKVEKVRKKQVSQTKI-----RVIS 235  
DB 133 CIVYGICGIPVTMIIANVGYLNFAGDSRRTKIEAVRQQRMSKASLAGKIYKESIQT 192  
QY 236 TILFILACIIVFVITPAVIFPKYIG-WTALESIVFVVVTLTVGFGDFVAGGNAGINRE 294  
DB 193 TSLALLCFLVLYAVGALLPLINGELDFNGLYFLCLTAIDFGOLVP-----IRV 245  
QY 295 WYKPLVFWIILVGLA-----ERRRLGLDQRAHSLDMLSPKRSVFAALDTRGFKASS 412  
DB 246 ELLPITFLVYICIGLAIITIAINISBYMKLHYGKMKNAQTRINFGGKTLKVRDLLH 305  
QY 324 VLSKTKTEVEGEIKAAHAAEWKANTABFETRRRLSVEIHDKIQRAATIRSM----- 375  
DB 306 AVGKCKGVEPMIDALDLENVVERTIAQEGREP-PEDLNDEPPREPSPRSIIHSPGSTR 364  
QY 376 -----ERRRLGLDQRAHSLDMLSPKRSVFAALDTRGFKASS 412  
DB 365 PSNPMPSPSPREDHPHFIFKVDAPAPRSLPLPAYELDI---KKPIQALSNEFWNQSA 420  
QY 413 QESINNRNNRLK-GPEQLNKH-----GQASEDNII-----NKFGSTSLRTR 456  
DB 421 QELFNLDLTQIEINTELVEDHKCESVIIIEPATFEDMTIQHSLCVEDYEREKVPKR 480  
QY 457 KKKDLKKTLPEDVOKIYKTRNYSLEBKKEETKMCNSDNSTAMLTDC 507  
DB 481 -FREKKYNGDPRKLYET---YOEWDRLERUSDKRGPRKRSVLNLSNC 527

RESULT 15  
T43357  
potassium channel chain n2p16 homolog - Caenorhabditis elegans  
C-species: Caenorhabditis elegans  
C-date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
C-accession: T43357  
R:Wang, Z.W.; Kunkel, M.T.; Wei, A.; Butler, A.; Salkoff, L.  
Ann. N. Y. Acad. Sci. 868, 286-303, 1999  
A:Title: Genomic organization of nematode 4TM K+ channels.  
A:Reference number: 422446; MUID:93342707; PMID:10414302  
A:Accession: T43357  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-555 <WAN>  
A:Cross-references: EMBL:AF083645; PIDN:AAC32856.1

Query Match 9.6%; Score 264; DB 2; Length 555;  
Best Local Similarity 20.3%; Pred. No. 1.1e-10;  
Matches 108; Conservative 94; Mismatches 205; Indels 124; Gaps 16;

QY 74 AIFVWVVLVTGVLVFRALPQPESSQKNTIALEKAEFLRDHVCVSPQBLETL----- 127  
DB 28 SLLMLVLLYSFLGGFIDRIETNAHEMK-----RNERINRTACVS-QILHSIHWSHN 80  
QY 128 ----IQHALDADNAGVSPIGNSSNNSHWDLGSAFFAGTVITTIYGNIAPESTGGKIF 183  
DB 81 QTHKVOVAEDIAC----FEPEKDERSEWNVFTATLYGFGIVTLTGYNRIAPITYTGRMF 136  
QY 184 CILYAIFGIPLFGFLAGIGDQGTIFGKSIAKVEKVRKKQVSQTKI-----RVIS 235

Db 137 CIVIGICGIPVTMIIANVQYLNFFAGDSRRKIEAYRQORMSKASLAGKIYKESSIOV 196  
Qy 236 TILFIIAGCIVFTIIPAVIFKYIEG-WTALESYFVVVTLTTVVGDFVAGNAGINYRE 294  
Db 197 TSLALLCVFLIYVAVGALLPLLENGELDFENGFLYFNFLCLTAIDFQQLVP-----IRV 249  
Qy 295 WYKPLVWFMLVGLA-----YFAVLVSMIGDWLR 323  
Db 250 ELLPITFLYVCIGLATTITAINIGSEYMKLHYWGKKMNAQAOTRIWFGCKTLKVRDLH 309  
Qy 324 VLSKTKEEYGEIKAHAAEWKANVTAEFRETRRLSVEIHDKLQRAATIRSM----- 375  
Db 310 AVGKCGVEPGMIDALDLENVVERTIAMQEGREP-PEDLNDEPPREPSPIIHSPCSTR 368  
Qy 376 -----ERRRLGLDQAHSLDMLSPKRSVFAALDTGRFKASS 412  
Db 369 PSNPPMSPPSPREDHPPIFKMDAPAPRSPPLPAYELDI-----KPFQALSNFNMQSA 424  
Qy 413 QESINNRPNRLRK-GPEQLNKH-----GQGASEDNII-----NKFGSTSLTKR 456  
Db 425 QEKLFDLDTFQIEINTELVEDHKCSVIIIEPPATFEDMTIQHSLCVEDYEREKVPKR 484  
Qy 457 KNKDLKXLPEDVQKIYKTFRNYSLEEKKEBETEKKXCNDSNSTAMLTDC 507  
Db 485 -FREKKEMVGRDPRKLYET---YQEEWDRLERLSDRKHGPRKSVLNLNSC 531

Search completed: June 29, 2004, 18:19:57  
Job time : 23 secs





Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	2578.5	93.4		535	11	Q8BW1	Q8bw1 mus musculus
2	2180.5	79.0		453	11	Q8BZ0	Q8bz0 mus musculus
3	1247.5	45.2		426	11	Q9Z0B6	Q9z0b6 rattus norv
4	1244.5	45.1		411	6	Q9HY88	Q9hy88 bos taurus
5	1242.5	45.0		411	4	Q9NRT2	Q9nr12 homo sapien
6	983.5	35.6		241	11	Q9CX88	Q9cx88 mus musculus
7	930	33.7		193	11	Q8BWJ6	Q8bwj6 mus musculus
8	778	28.2		397	11	Q92414	Q92414 rattus norv
9	478.5	17.3		502	11	Q9JK62	Q9jk62 mus musculus
10	434	16.4		257	11	Q80X50	Q80x50 mus musculus
11	447	16.2		184	4	Q8N4V5	Q8n4v5 homo sapien
12	424.5	15.4		341	6	Q8HZT2	Q8hz12 bos taurus
13	403	14.6		307	13	Q801T4	Q801t4 xenopus lae
14	400	14.5		336	11	Q9Z2T2	Q9z2t2 rattus norv
15	398	14.3		344	11	Q8R454	Q8r454 cavia porce
16	395.5	14.3		336	11	Q99L39	Q99l39 mus musculus



```
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 426 AA; 46912 MW; CACDA05BB95FDBEC CRC64;

Query Match
  45.2%; Score 1247.5; DB 11; Length 426;
Best Local Similarity 63.8%; Pred. No. 3.7e-83;
Matches 245; Conservative 56; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVQPKSATNGQPPAPAPTPTPLRLSSISRAATVA-RMEGTSQGLQTVMKWTVAI 75
DB 17 AAPDLLDPKSA-----AQNSKPLSPSAKPTVLASRVESDS-----AINVMKWTVTI 65

QY 76 FVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQIHALDAD 135
DB 66 FLVVVLYLIIGATVFRALQEPQISQRTTIVIQKQNFIAQHACVNSTDELQIQTVAI 125

QY 136 NAGVSPFGNSNNSHWDLGSAFFAGTVITTIYGNIAPISTEGGKIFCILYALFIPPLF 195
DB 126 NAGIIPLGNSNSQVSHWDLGSSFFAGTVITTIYGNISPRTEGGKIFCIIYALLGIPPLF 185

QY 196 GFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFLLAGICVFTTIPAVIF 255
DB 186 GFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFLLAGICVFTTIPAVIF 245

QY 256 KYIEGWTALSIYFVVVTLTTVFGDFVAGGNAGINREWKPLVFWFVLVGLAYFAAVL 315
DB 246 KHIEGWSALDAIYFVVVTLTTVFGDFVAGG-SDIEYLDYFKPVVFWFVLVGLAYFAAVL 304

QY 316 SMIGDMLRVLSKTKKEVEGKIAHAAEKANKVTAEPRETRRLSVIHDKLORAATIRSM 375
DB 305 SMIGDMLRVLSKTKKEVEGKIAHAAEKANKVTAEPRETRRLSVIHDKLORAATIRSM 361

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
DB 362 -KRKLSAELAGNHQELTPCRTL 384

RESULT 4
Q8HY88 PRELIMINARY; PRT; 411 AA.
ID Q8HY88
AC Q8HY88
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Potassium channel subfamily K member 2.
GN KCKN2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RX PubMed=12368289;
RA Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
RT "An ACTH- and ATP-regulated background K+ Channel in Adrenocortical
RL J. Biol. Chem. 277:49186-49193 (2002).
DR EMBL; AY148474; AAN37591.1; -.
DR GO; GO:0015020; C:membrane; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;

Query Match
  45.1%; Score 1244.5; DB 6; Length 411;
```

```
Best Local Similarity 63.5%; Pred. No. 5.8e-83;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVQPKSATNGQPPAPAPTPTPLRLSSISRAATVA-RMEGTSQGLQTVMKWTVAI 75
DB 2 AAPDLLDPKSA-----AQNSKPLSPSAKPTVLASRVESDT---TINVMKWTVTI 50

QY 76 FVVVVVLTGGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTILQIHALDAD 135
DB 51 FLVVVLYLIIGATVFRALQEPHEISQRTTIVIQKQNFISQHACVNSTDELQIQTVAI 110

QY 136 NAGVSPFGNSNNSHWDLGSAFFAGTVITTIYGNIAPISTEGGKIFCILYALFIPPLF 195
DB 111 NAGIIPLGNSNSQVSHWDLGSSFFAGTVITTIYGNISPRTEGGKIFCIIYALLGIPPLF 170

QY 196 GFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFLLAGICVFTTIPAVIF 255
DB 171 GFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFLLAGICVFTTIPAVIF 230

QY 256 KYIEGWTALSIYFVVVTLTTVFGDFVAGGNAGINREWKPLVFWFVLVGLAYFAAVL 315
DB 231 KHIEGWSALDAIYFVVVTLTTVFGDFVAGG-SDIEYLDYFKPVVFWFVLVGLAYFAAVL 289

QY 316 SMIGDMLRVLSKTKKEVEGKIAHAAEKANKVTAEPRETRRLSVIHDKLORAATIRSM 375
DB 290 SMIGDMLRVLSKTKKEVEGKIAHAAEKANKVTAEPRETRRLSVIHDKLORAATIRSM 346

QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399
DB 347 -KRKLSAELAGNHQELTPCRTL 369

RESULT 5
Q9NRT2 PRELIMINARY; PRT; 411 AA.
ID Q9NRT2
AC Q9NRT2
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Two-pore domain potassium channel TREK-1.
GN TREK-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20244931; PubMed=10784345;
RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA Medhurst A.D., Murdoch P., Chapman C.G.;
RT "Cloning, localisation and functional expression of the human
RT orthologue of the TREK-1 potassium channel.";
RL Pflugers Arch. 439:714-722(2000).
DR EMBL; AF171068; AAF89743.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 411 AA; 45494 MW; FDB40CAB21B42A1C CRC64;

Query Match
  45.0%; Score 1242.5; DB 4; Length 411;
Best Local Similarity 63.5%; Pred. No. 8.2e-83;
Matches 244; Conservative 57; Mismatches 66; Indels 17; Gaps 5;

QY 17 AAAPVQPKSATNGQPPAPAPTPTPLRLSSISRAATVA-RMEGTSQGLQTVMKWTVAI 75
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Db      2  AAPDLLDPKSA-----AQNSKPRLSFSTKPTVSLASRVESDT---TINVMKWKTVSTI 50
QY      76  FVVVVVYLVGGLVFRALPEQPESSOKNTIALEKAEFLRDHVCVSPQSELETLIOHALDAD 135
Db      51  FLVVVYLIIGATVFKALEQPEHSIQRTTIVIQKOTTFISQHCNVNTELDSELIQIVAAI 110
QY     136  NAGVSPIGNSSNNSHWDLGSAFFAGVTTTIGVGNIAPTSTEGKIPCIILYAIPIPLF 195
Db     111  NAGIIPLGNTSNQISHWDLGSSFFPAGVTTTIGFNGISPRTEGGKIPCIILYALLGIPLF 170
QY     196  GFLLAGIGDGLTIFGKSIARVEKVKQVRSQKIRVISTILRTLAGCIVFVTPAVIF 255
Db     171  GFLLAGVGDGLTIFGKSIARVEKVKQVRSQKIRVISTILRTLAGCIVFVTPAVIF 230
QY     256  KYIEGWTALIESYFVVVLTITVTFGDFVAGNAGINRYEMKPLVFWILVGLAYFAVL 315
Db     231  KHIEGWSALDAIFYFVVITLTITGFDYVAGG-SDIEYLDYFKPVVFWILVGLAYFAVL 289
QY     316  SMIGDMLVLSKTKKEVEGEIKAHAAEWKANVTAEFRTRRLSVSEIHDKLOAATIRSM 375
Db     290  SMIGDMLRVISKTKKEVEGEFRHAAEAETANVTAEFRTRRLSVSEIHDKLOAATIRSM 346
QY     376  ERRRLGLDORAHSLDMLSPKRSV 399
Db     347  -KKLSAELAGNHQELTPCORTL 369

RESULT 6
Q9CX88      PRELIMINARY;      PRT;      241 AA.
AC Q9CX88;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE 3010005K24RIK protein.
GN 3010005K24RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Saito R.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Donato M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK019376; BAB31686.1;
DR MGD; MGI:1924704; 3010005K24RIK.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005267; P.potassium channel activity; IEA.
DR GO; GO:0006813; P.potassium ion transport; IEA.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01499; TREKCHANNEL.
SQ SEQUENCE 241 AA; 25799 MW; B4C39F77CD0A39DA CRC64;

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Query Match      35.6%; Score 983.5; DB 11; Length 241;
Best Local Similarity 93.4%; Pred. No. 3.9e-64;
Matches 197; Conservative 3; Mismatches 4; Indels 7; Gaps 2;

QY 13 VAVPAAA-PVCPKSAATNGQPAPAPPTPRLSSISSRATVVARMEGTSGGGLQTVMKWKT 71
Db 18 VAVPAAAAPPVCPKSAATNGH-----HPVPRLSISSRATVVARMEGASQGGIQTVMKWK 71
QY 72 VVAIFVVVVVYLVGGLVFRALPEQPESSOKNTIALEKAEFLRDHVCVSPQSELETLIOHA 131
Db 72 VVAIFVVVVVYLVGGLVFRALPEQPESSOKNTIALEKAEFLRDHVCVSPQSELETLIOHA 131
QY 132 LDADNAGVSPIGNSSNNSHWDLGSAFFAGVTTTIGVGNIAPTSTEGKIPCIILYAIPIFG 191
Db 132 LDADNAGVSPGVGNSSNNSSSHWDLGSAFFAGVTTTIGVGNIAPTSTEGKIPCIILYAIPIFG 191
QY 192 IPLFGLLAGIGDGLTIFGKSIARVEKVKR 222
Db 192 IPLFGLLAGIGDGLTIFGKSIARVEKVKR 222

RESULT 7
Q8BWJ6      PRELIMINARY;      PRT;      193 AA.
AC Q8BWJ6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Potassium channel subfamily K member 10 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052327; BAC34939.1;
FT NON_TER
SQ SEQUENCE 193 AA; 22174 MW; 8CCBADA59EF60641 CRC64;

Query Match      33.7%; Score 930; DB 11; Length 193;
Best Local Similarity 93.8%; Pred. No. 2.4e-60;
Matches 181; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 346 NVTAEFRETRRLSVSEIHDKLOAATIRSMERRLGLDORAHSLDMLSPKRSVFAALDT 405
Db 1 NVTAEFRRRLSVSEIHDKLOAATIRSMERRLGLDORAHSLDMLSPKRSVFAALDT 60
QY 406 GRFKASSQESINRNPNLRLKPGQLKNGHOGASEDNINKFGSTSRITKRNKDLKKTL 465
Db 61 GRFKASSQESINRNPNLRLKPGQLTKHGOGASEDNINKFGSTSKITKRNKDLKKTL 120
QY 466 PEDVQKIYKTRNYSLDEEKEEETKCMKNSDNSTAMLTDCIOQHALENGMTPTTKD 525
Db 121 PEDVQKIYKTRNYSLDEEKEEETKCMKNSDNSTAMLTDCIOQHALENGMTPTTKD 180
QY 526 REPENNSLLEDRN 538
Db 181 QGLENNLSLEDRN 193

RESULT 8
Q92414      PRELIMINARY;      PRT;      397 AA.
AC Q92414;
DT 01-DEC-2001 (TRENBLrel. 19, Created)

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DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Mechanosensitive tandem pore potassium channel.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=21268449; PubMed=11374070;
RA Kim Y., Bang H., Gnatenko C., Kim D.;
RT "Synergistic interaction and the role of C-terminus in the activation
RT of TRAAK K+ channels by pressure, free fatty acids and alkali.";
RL Pflugers Arch. 442:64-72(2001).
DR EMBL; AF302842; AAK60504.2; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR001990; Granin.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR008074; TRAAK_channel.
DR Pfam; PF01271; Granin_1.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01691; TRAAKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 397 AA; 42987 MW; 3AF04C43FA982D22 CRC64;

Query Match      28.2%; Score 778; DB 11; Length 397;
Best Local Similarity 51.2%; Pred. No. 9.2e-49;
Matches 150; Conservative 56; Mismatches 81; Indels 6; Gaps 3;

QY 67 MKWTVVAFVWVYVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQLETL 126
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MRSTTALLALLVLLVSGALVFYALEQPHQVQKQEDGDRDQFLKHPCVSKNLEG 60

QY 127 LIQHLDADNAGVSP---IGNSSNNSHWDLGSAPFFAGVITTTIGVNIAPSTEGGKIF 183
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 FIKLVALGCGGANFETSWTNSNHSAMWLGSAFFPSGFIITTTIGVNIALTDAGRLF 120

QY 184 CILYAFGILPFLGAGIDGLTGIFGKSIAREVKVFRRKQVSOQKIRVISTILFILAG 243
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 CIFVALVGIPLFGMLLAGVDRGLSSLRGGIEHAEVFLKWHVPPGLVRLMSAVLELLIG 180

QY 244 CIVFTTIPAVIFKXIEGWTALESITYFVVTITTTGCGDFVAGNAGINYEWKPLVWF 303
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 CLFLVLTPTTFVFSYMSKSLKALYFVITVLTGFGDYVPGDGTGON-SPAQLVWF 239

QY 304 ILVGLYFAAVLMSIGDLRLVLSKTKKEVGEIKAHAAEWKANVTAEFFRETR 356
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
240 ILFGLAFASVFTTIGNLRAVSERTRAENGGLTAQAASWTGTVA--RVTQR 290

RESULT 9
Q9JK62 PRELIMINARY; PRT; 502 AA.
AC Q9JK62.
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Potassium channel TASK2 (TASK2 potassium channel).
GN KCNK5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ; TISSUE=Kidney;
RA Roux J., Barhanin J.;
RT "Mouse two P domain potassium channel TASK2.";
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Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RA Cid L.P., Niemeyer M.I., Sepulveda F.V.;
RT "Functional properties of mouse TASK-2 potassium channel.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF259395; AAF68668.1; -.
DR EMBL; AF319542; AAG35065.1; -.
DR EMBL; AK085330; BAC39423.1; -.
DR MGD; MGI:1336175; Kcnk5.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003092; TASK channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 502 AA; 55976 MW; E4C7E7CC71B44D95 CRC64;

Query Match      17.3%; Score 478.5; DB 11; Length 502;
Best Local Similarity 27.0%; Pred. No. 1.2e-26;
Matches 126; Conservative 76; Mismatches 185; Indels 79; Gaps 13;

QY 79 VVYVLTGGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQLETLIQLHLDADNAG 138
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 IIFYLAIGAAIFEVLEEPEHKEAKNYITQKHLKSPCLSQEGDKILQVSDAADQG 71

QY 139 VSPIGNSSNNSHWDLGSAPFFAGVITTTIGVNIAPSTEGGKIFCILYAFILPFLGFL 198
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
72 VAITGNQTFN--NWNWPNAMIFAAITTTIGVNVAPKTPAGRLFCVFGVGLFVPL--C 126

QY 199 LAGIDGLTGIFGKSIAREVKVFRRKQVSOQKIRVISTILFILAGCTIVTIPAVIFKVI 258
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
127 LTWI--SALGKFFGGRAGELGQFLTRRGVSLRAQAQITCTAIFVWGLVHLVIPPVFVMT 185

QY 259 EGWTALESITYFVVTITTTGCGDFVAGNAGINYEWKPLVWFVILYGLAYFAAFLSMI 318
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
186 EEWNYIEGLYISFTITSTIGDFVAGNPNANYHALYRYFVELWYLGLA----- 236

QY 319 GDWLRVLSKTKKEVGEIKAHAAEWKANVTAEFFRETRRLSVIEIHKLQRAATIRSMERR 378
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
237 --WLSIF-----VNKVS-----MFVEVHKAIK-----KRRRRR 263

QY 379 RLGLDQRAHSLDMSPEKRSVPAALDTCRFRASSOESINRRNNL-----RLK 426
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
264 KESFESSPESRKALQWAGSTASKDVNIFPSLKSEETNDLIKQIKKAMKTSGGGERVP 323

QY 427 GPEQLMKHGGQASEDNIINKFGSTRLTKRKNKDKLTLPEDVQKIYTFRRNYSLEDEKK 486
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
324 GP----GHGLPGQGRDLPTIPASLAPLVVYS---KNRVP-SLEEVSOQLKXKHGVSRLP 374

QY 487 EEETEKCNDNSNSTAML-----TDCIQHAELENGMIPTDTKDREP 528
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
375 GEEAGAAQPKDSYQTSVEVFINQLDRISEGE-----PWEALDYHP 414

RESULT 10
Q80XE0 PRELIMINARY; PRT; 257 AA.
ID Q80XE0
AC Q80XE0;
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DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Similar to potassium channel, subfamily K, member 5 (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC051088; AAH51088.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0008813; F:potassium ion transport; IEA.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_1pore.  
 DR PRINTS; PR01333; 2POREKCHANEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 KW Ionic channel.  
 FT NON\_TER 257  
 SQ SEQUENCE 257 AA; 29001 MW; AA00FB04152126C4 CRC64;

Query Match 16.4%; Score 454; DB 11; Length 257;  
 Best Local Similarity 37.4%; Pred. No. 3e-25;  
 Matches 91; Conservative 47; Mismatches 95; Indels 10; Gaps 4;  
 QY 79 VVYLVTGGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHALDADNAG 138  
 DB 12 IIFYLAIAGAAIFVELEPHWEAKQVYTKLHLKEPPCLSGDLKILQVWSDAQQ 71  
 QY 139 VSPIGNSSNSHDLSGAPFFACTVITIGYGNIAPESTEGGKIFCILYAFIPIGFL 198  
 DB 72 VAITGNQTFN--NMWPNAMIFATVITIGYGNVAPKTPAGRLFCVYGLFGVPL--C 126  
 QY 139 LAGIGDQLGTIFGKSIARVEKVKQVSPQKIRVISTIFILAGCIVFVTIPAVIFKYI 258  
 DB 127 LTWI-SALGKFFGGRAKELGQFLTERGVSLRKAQITCTAIFVWGLVHLVFPFVEMV 195  
 QY 259 EGNWALESIYFVVTITVTTGDFVAGNAGINREWKPLVFWIUVGLYFAAVLSMI 318  
 DB 186 EEWNYIEGLYSFTISTIGDFVAGNPSANYHALRYFVELWYIYGLAW---LSLF 241  
 QY 319 GDW 321  
 DB 242 VNW 244

RESULT 11  
 ID Q8N4V5 PRELIMINARY; PRT; 184 AA.  
 AC Q8N4V5;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DE Similar to potassium channel, subfamily K, member 4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC033577; AAH33577.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.

DR GO; GO:0006813; F:potassium ion transport; IEA.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003976; Trek channel.  
 DR PRINTS; PR01499; TREKCHANNEL.  
 KW Ionic channel.  
 SQ SEQUENCE 184 AA; 19380 MW; A96A6B586D40AFF0 CRC64;  
 Query Match 16.2%; Score 447; DB 4; Length 184;  
 Best Local Similarity 44.8%; Pred. No. 6.1e-25;  
 Matches 91; Conservative 29; Mismatches 54; Indels 30; Gaps 2;  
 QY 20 PVCQKPSATNGQPPAPAPPTPTPLSISRRATVVARMEGTSGGLQTVMKWKTWVAIFVV 79  
 DB 8 PPARPLQAGSGAGPAG-----RAMSTTLLALLALV 39  
 QY 80 VVYLVTGGLVFRALQPFESSQKNTIALEKAEFLRDHVCVSPQELTILQHALDADNAGV 139  
 DB 40 LLYLVSGALVFRALQPFHQRELGVEVREKFLRAHPCVSDQELGLLTKVADALGGGA 99  
 QY 140 SPIGNSSNSSH--WDLGSAPFFAGTVITIGYGNIAPESTEGGKIFCILYAFIPIGFL 197  
 DB 100 DPESTNSTSSSHAWDLGSAPFFAGTVITIGYGNIAPESTEGGKIFCILYAFIPIGFL 159  
 QY 198 LLAGIGDQLGTIFGKSIARVEKVF 221  
 DB 160 LLAGVGRDLGSLRHGIGHIEAIF 183

RESULT 12  
 ID Q8HZT2 PRELIMINARY; PRT; 341 AA.  
 AC Q8HZT2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Potassium channel TASK-4.  
 GN KCNK17.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Derst C., Renigunta V.K., Preisig-Mueller R., Rajan S., Daut J.;  
 RT "Cloning and sequencing of bovine potassium channel TASK-4";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF479760; AAN32894.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005267; F:potassium channel activity; IEA.  
 DR GO; GO:0008813; F:potassium ion transport; IEA.  
 DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003092; TASK channel.  
 DR PRINTS; PR01333; 2POREKCHANEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 SQ SEQUENCE 341 AA; 37695 MW; 0A21FEEA71B39401 CRC64;

Query Match 15.4%; Score 424.5; DB 6; Length 341;  
 Best Local Similarity 34.2%; Pred. No. 6.4e-23;  
 Matches 96; Conservative 58; Mismatches 120; Indels 7; Gaps 4;  
 QY 39 PTPRLSISRRATVVARMEGTSGGLQ-TVMKWTWVAIFVVVYVTGGVAFRALEQPF 97  
 DB 3 PDSRLS-ASPAKSGRAWNASERGQCAVPVPSTLLLLLTLYLTLYLTGTCVFWALSSPA 61  
 QY 98 ESSQKNTIALEKAEFLRDHVCVSPQELTILQHALDADNAGVSPIGNSSNSHWDLSGA 157  
 DB 62 AHDSSKRFQDKWALLRNFTCLDQALDSLIRGIEAVKNGDIVLGNTT-SMGRWEFVGS 120  
 QY 158 PFACTVITIGYGNIAPESTEGGKIFCILYAFIPIGFLLAGIGDQLGTIFGKSIARV 217  
 DB 121 PFFSVSTTITIGYGNLSPTWALRFCTFFALVGIPLNLVVL----NRLGHCMQGVHRC 176

```
QY 218 EKVFRRKQVSTQKIRVISTILFACIVFVTPAVIFKYIEGWTALSIYFVWVTLTV 277
DB 177 ARRLGAWKDPKARWLACSSALLSGLLFLLLPLLFNHEGWTWVEGFVSFTLSTV 236
QY 278 GFGDFVAGNAGINREWTGKPLVFWFVLVGLAYFAVLMSI 318
DB 237 GFGDYVGNPNRNYPLWYQNTVSLWFLFMAWLALIILKI 277

RESULT 13
Q80174 PRELIMINARY; PRT; 307 AA.
AC Q80174;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to potassium channel, subfamily K, member 6 (TWIK-2).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC047247; AAH47247.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR001779; TWIK1 channel.
DR InterPro; IPR005408; TWIK1 channel.
DR InterPro; IPR005408; TWIK1 channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1096; TWIK1CHANNEL.
DR PRINTS; PRO1586; TWIKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 307 AA; 35190 MW; E7C4B8B553B94BE9 CRC64;

Query Match 14.6%; Score 403; DB 13; Length 307;
Best Local Similarity 35.2%; Pred. No. 2.1e-21;
Matches 86; Conservative 50; Mismatches 98; Indels 10; Gaps 4;

QY 69 WKTVAIFVWVYVLTGGLVFRALEQPFSSQKNTTIALEKAEFLRDHVCVSPQLETLI 128
DB 4 WLLTLVVCVYVILLGALVISIESPYEASLRDELRLQKNVFNESPCNVSSLEAFL 63
QY 129 QHALDADNAGVSPIGNSNSSHWDLGSAFFAGTAVTTTIGYGNIAPISTEGGKIFCILIYA 188
DB 64 EKIINANKYGVSVLHNASNDSK-WDIASSLFFASTLVTTGYGTYTTLTDSGKAFICFYG 122
QY 189 IFGTLPGFLIAGIDGLGTFEGKSIAR--VEKVPFRKQVSTQKIRVISTILFILAAGCI 245
DB 123 LIGVFTMLVSSVFQRLMWNFTHKPIRYLQVHGFPKRWVQ-----LHFIFLLLVFV 177
QY 246 VFTVTPAVIFKYIE-GWTALESIFYVWVTLTVTGFVAGNAGINREWTGKPLVFWFI 304
DB 178 FFLIIPSAFNITETNSFLDAFYFCFISLCTIGLDYVPGEQNDQWLRLKLYKVSAYFL 237
QY 305 LVGL 308
DB 238 FVGL 241

RESULT 14
Q922T2
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Q922T2 PRELIMINARY; PRT; 336 AA.
AC Q922T2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative potassium channel TWIK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K.;
RT "Cloning and localization of rTWIK, a putative potassium channel with
RT two P domains.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022819; AAD09336.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; P:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR001779; TWIK1 channel.
DR InterPro; IPR005408; TWIK1 channel.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1096; TWIK1CHANNEL.
DR PRINTS; PRO1586; TWIKCHANNEL.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;

Query Match 14.5%; Score 400; DB 11; Length 336;
Best Local Similarity 30.5%; Pred. No. 3.9e-21;
Matches 100; Conservative 60; Mismatches 108; Indels 60; Gaps 11;

QY 76 FVVV--VYVLTGGLVFRALEQPFSSQKNTTIALEKAEFLRDHVCVSPQLETLIHALD 133
DB 25 FLVLGLLYLVFGAVFSSVELPYEDLLRQELRKRRFLEEHECLSPQLGRLVLE 84
QY 134 ADNAGVSPIGNSNSSHWDLGSAFFAGTAVTTTIGYGNIAPISTEGGKIFCILIYAIFGP 193
DB 85 ASNYGVSVLSNAGSN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIVSIGIP 143
QY 194 LFGFLLAGIDGLGTFEGKSIARVEKVRKQV-----SQTQKIRVISTIL--FILA 242
DB 144 FTLLFLTAV-----VQRTVTVTRRVPVLYFHIRWGFSKQVVAIVHAVLLGFTVTV 192
QY 243 GCIVFTTIPAVIFKYIE-GWTALESIFYVWVTLTVTGFVAGNAGINREWTGKPLVW 301
DB 193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLDYVPGEGYNQKRELKIGIT 250
QY 302 FWILVGLAYFAVLMSIGDLRVLSK-----KTKEVGEIKAAHAAEWKANVTAEPRETR 356
DB 251 CYLLGLLIAMLVLETFCE-LHELKFRKMFYVKKDKEDQVHME----- 295
QY 357 RLSVFIHDKL-----QRAATIRSMERR 378
DB 296 -----HDQLSPSSITEQAAGLKEEQK 317

RESULT 15
Q8R454 PRELIMINARY; PRT; 336 AA.
AC Q8R454;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Potassium channel TWIK-1.
OS KCNK1.
OC Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
```

```
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Derst C., Rajan S., Preisig-Mueller R.;
RT "Cloning and sequencing of guinea pig TWIK channels.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075096; AAL82795.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:005216; F: ion channel activity; IEA.
DR GO; GO:005267; F: potassium channel activity; IEA.
DR GO; GO:000813; F: potassium ion transport; IEA.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR InterPro; IPR001779; TWIK1 channel.
DR InterPro; IPR005408; TWIK channel.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01096; TWIK1CHANNEL.
DR PRINTS; PR01586; TWIKCHANNEL.
KW Ionic channel; Transmembrane.
SQ SEQUENCE 336 AA; 38102 MW; 299B69159D7F5B2A CRC64;

Query Match      14.4%; Score 398; DB 11; Length 336;
Best Local Similarity 29.8%; Pred No. 5.5e-21;
Matches 96; Conservative 60; Mismatches 108; Indels 58; Gaps 10;

QY      80 VYLVVGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQBLETLIQHALDADNAGV 139
Db      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      31 LLYLVGAVVFSVVELPYEDLLRQELRKLKRRFLREHECLSEPOLQFLGRVLEASNYGV 90
Db      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      140 SPIGNSSNNSSHDGLGSAFFAGTVITTTIGYNTAPSTEGGKIFCIILYAIKPIPLGFI 199
Db      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      91 SVLSNAGN-WNWDFTSALFFASTVLTSTGYGHTVPLSDGGKAFCIISVIGIPFTLLFL 149
Db      ::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY      200 AGIGDQLGTFKSIARVERKRVKQV-----SQTKIRVISTIL--FILAGCIVFV 248
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      150 TAV-----VQRITVHVRPVLVFIHWGFSKQWGIHVAVLGFVTVSCFFP- 197
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      249 TIPAVIFKYIE-GWTALESIVVVVTLTVGFGDPVAGGNAGINREWYKPLVWFVILVG 307
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      198 -IPAAVSVLEDDWNFLSFYFCFISLSTIGLDYVFGEGYNQKRFELXIGITCYLLLG 256
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      308 LAYFAAVLSMIGDMLRVLSK-----KTKEEVEYKKAHAAEWKANVTAEFRETRRLSVEI 362
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      257 LIAMLVLETCE-LHELKPKRMFYVKDKDQDVHIVE----- 295
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      363 HDKL-----QRAATIRSMERR 378
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
QY      296 HDQLSFSSITDQAAASVKEQKQ 317
Db      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
```

Search completed: June 29, 2004, 18:19:23  
Job time : 47 secs



Result No.	Query No.	Score	Match	Length	DB	ID	Description
1		2760	100.0	538	5	AA847930	Human TRE
2		2760	100.0	538	5	AA616596	Human TWI
3		2760	100.0	538	5	ABP69333	Human pol
4		2697	97.7	543	5	AA211804	Human TRE
5		2697	97.7	543	5	AAU81354	Novel hum
6		2697	97.7	543	5	AAU79472	Human nov
7		2697	97.7	543	5	AB883842	Human nov
8		2697	97.7	543	6	ADA05746	Hypothala
9		2697	97.7	543	7	ADE08315	Human NOV
10		2693	97.6	543	5	AAU79473	Novel pro
11		2657.5	96.3	724	5	AA014193	Human nov
12		1630	59.1	383	4	ABG02731	Human tra
13		1412.5	51.2	557	4	ABG08305	Novel hum
14		1251.5	45.3	411	3	AAE10342	Novel hum
15		1248.5	45.2	411	2	AAU28497	Mouse h-T
16		1247.5	45.2	370	2	AAU30648	Mouse h-T
17		1243	45.0	411	3	AAE10341	A mechani
18		1242.5	45.0	411	2	AAU34133	Human TRE
19		1242.5	45.0	411	2	AAU28496	Human pot
20		1242.5	45.0	411	4	AAE50044	h-TREK1 p
21		1235	44.7	411	5	AAE16597	Human TRE
22		1218.5	44.1	426	4	AAU07622	Human TWI
23		1218.5	44.1	426	4	AAU07618	Human pot
24		1214.5	44.0	426	4	AAU07623	Human pot
25		1210.5	43.9	426	4	AAU07625	Human pot

Claim 3; Page 44-46; 50pp; English.

This sequence shows a protein, which constitutes a human K<sup>+</sup> channel, TREK2, which has two pore domains that produces currents whose current-voltage relationship is slightly inwardly rectifying in high symmetrical K<sup>+</sup> conditions. TREK2 is activated by general anaesthetics at clinical concentrations. It is modulated by different types of neurotransmitter receptors. The TREK2 gene produces a cDNA of 2730 bp which contains an open reading frame of 1617 nucleotides. The TREK2 protein has the same overall structure as previously described K<sup>+</sup> channels. It has four membrane spanning domains (M1-M4), two pore domains (P1-P2) and an extended loop between M1 and P1. TREK2 shares 63% identity and 78% homology to TREK1. The chromosomal location of the TREK2 gene is 14q31. TREK2 is useful in methods for screening various compounds. In particular, the protein is useful in methods for identifying biologically active compounds with anaesthetic properties

Sequence 538 AA;

Query Match	100.0%;	Score	2760;	DB	5;	Length	538;
Best Local Similarity	100.0%;	Pred. No.	6e-244;				
Matches	538;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

QY 1 MFFLYTDFFLSIVAPAAAPVCQPKSATNQPPAPAPPTPRLSISSRATVVARMEGTSQ 60  
 DB 1 MFFLYTDFFLSIVAPAAAPVCQPKSATNQPPAPAPPTPRLSISSRATVVARMEGTSQ 60  
 QY 61 GGLQTVMKWKTVAIFVWVVVYLTGGLVFPRALEQPPESQKNTIALEKAEFLRDHVCVS 120  
 DB 61 GGLQTVMKWKTVAIFVWVVVYLTGGLVFPRALEQPPESQKNTIALEKAEFLRDHVCVS 120  
 QY 121 POELFTLIQHALDADNAGVSPIGNSNSSSHWDLGSAFFPAGTVITTIYGXNIAPSTEGG 180  
 DB 121 POELFTLIQHALDADNAGVSPIGNSNSSSHWDLGSAFFPAGTVITTIYGXNIAPSTEGG 180  
 QY 181 KIFCILYAIFGPIFGFLGAGIGDQGTIFGKSIARVEKVFRRKQVQSQTIRVISTILFI 240  
 DB 181 KIFCILYAIFGPIFGFLGAGIGDQGTIFGKSIARVEKVFRRKQVQSQTIRVISTILFI 240  
 QY 241 LAGCIVFVTIIPAVIFKYIEGTALESIFYVVVTLTTVVGDFVAGNAGINTREWKPLV 300  
 DB 241 LAGCIVFVTIIPAVIFKYIEGTALESIFYVVVTLTTVVGDFVAGNAGINTREWKPLV 300  
 QY 301 NFWIILVGLAYFAAULSMIGDLRLVLSKTTKEEVGEIKAHAAEWKANVTAEPRETRRLSV 360  
 DB 301 NFWIILVGLAYFAAULSMIGDLRLVLSKTTKEEVGEIKAHAAEWKANVTAEPRETRRLSV 360  
 QY 361 EYHDKLQAAATIRSNERRRIGLDQRAHSLDMLSPKRSVFAALDTRGFKASSQESINRRP 420  
 DB 361 EYHDKLQAAATIRSNERRRIGLDQRAHSLDMLSPKRSVFAALDTRGFKASSQESINRRP 420  
 QY 421 NNRLKGPQLNKHGQGA SEDNIINKFGTSIRLTTRKNKDLKKTLPEDVQKIYKTFRNY 480  
 DB 421 NNRLKGPQLNKHGQGA SEDNIINKFGTSIRLTTRKNKDLKKTLPEDVQKIYKTFRNY 480  
 QY 481 LDEEKKBEETKMCNDNSSTAMLTDCIQOHAELNGMIPTDTKDREPNNSLLEDNRN 538  
 DB 481 LDEEKKBEETKMCNDNSSTAMLTDCIQOHAELNGMIPTDTKDREPNNSLLEDNRN 538

RESULT 2  
 AAE16596  
 ID AAE16596 standard; protein; 538 AA.  
 XX AAE16596;  
 DT 18-APR-2002 (first entry).  
 XX Human TWIK-Related K<sup>+</sup> channel-2 (TREK-2) protein.  
 DE Human TWIK-Related K<sup>+</sup> channel-2; TREK-2; anaesthetic; chromosome 14q31;  
 KW screening.

QY 241 LAGCIVFVTIPAVIFKYIEGWTALLESYFVVVTLTTVGDFGVAGNAGINREWKPLV 300  
DB 241 LAGCIVFVTIPAVIFKYIEGWTALLESYFVVVTLTTVGDFGVAGNAGINREWKPLV 300  
QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKTEEVGEIKAHAAEWKANTVAEPRETRRLSV 360  
DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKTEEVGEIKAHAAEWKANTVAEPRETRRLSV 360  
QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
QY 421 NNRLKGPPEQLNKHGQASDNIINKFGTSRLTKRKNKDLKKTLPEDVQKIYKTRFNY 480  
DB 421 NNRLKGPPEQLNKHGQASDNIINKFGTSRLTKRKNKDLKKTLPEDVQKIYKTRFNY 480  
QY 481 LDEEKEEBETEKMNCNSDNTAMLTDCIQOHAELNGMIPTDTKDREPENNSLLEDRN 538  
DB 481 LDEEKEEBETEKMNCNSDNTAMLTDCIQOHAELNGMIPTDTKDREPENNSLLEDRN 538  
RESULT 3  
ABP69333  
ID ABP69333 standard; protein; 538 AA.  
AC ABP69333;  
XX  
XX  
DT 20-JAN-2003 (first entry)  
DE Human polypeptide SEQ ID NO 1380.  
XX Human; genome mapping; Gene therapy; food supplement; virus; fungus;  
XX cell-proliferative disorder; neurodegenerative disease; bacterial;  
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;  
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
XX arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
XX haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
XX antiarthritic.  
OS Homo sapiens.  
XX  
XX WO200270539-A2.  
XX  
XX 12-SEP-2002.  
XX  
XX 05-MAR-2002; 2002WO-US005095.  
XX  
XX 05-MAR-2001; 2001US-00799451.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Zhou P, Goodrich BW, Asundi V, Zhang J, Zhao QA, Ren F;  
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
XX Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
XX WPI; 2002-759812/82.  
XX  
XX N-PSDB; ABZ11550.  
XX  
XX  
XX New polynucleotides comprising sequences assembled from expressed  
XX sequence tags (ESTs), useful for treating cell-proliferative,  
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
XX or coagulation disorders.  
XX  
XX Claim 9; SEQ ID NO 1380; 1012pp + Sequence Listing; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) comprising a  
XX nucleotide sequence selected from any of 948 sequences (ABZ1119-  
XX ABZ12066) or their mature protein coding portion, active domain coding  
XX protein or complementary sequences. The polynucleotides are useful for  
XX identifying expressed genes or for physical mapping of human genome. The  
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
XX markers, as a food supplement, for generating antibodies, in medical

CC imaging, screening and diagnostic assays and for treating cell-  
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
CC or lung fibrosis infections (bacterial, viral, fungal, parasitic),  
CC arthritis, etc. Note: the sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIFO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 538 AA;  
Query Match 100.0%; Score 2760; DB 5; Length 538;  
Best Local Similarity 100.0%; Pred. No. 6e-244;  
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFFLYTDFLSLVAVFAAAAPVCQPKSATNGOPPAPAPPTPRLSISSTVAVRMETGTSQ 60  
DB 1 MFFLYTDFLSLVAVFAAAAPVCQPKSATNGOPPAPAPPTPRLSISSTVAVRMETGTSQ 60  
QY 61 GGLQTVMKKTVAIFVWVVLVTGGVAFRALQPPRESSOKNTTALKAFLRDHVCVS 120  
DB 61 GGLQTVMKKTVAIFVWVVLVTGGVAFRALQPPRESSOKNTTALKAFLRDHVCVS 120  
QY 121 POELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAPFFAGTIVTTIGYGNIAPESTEGG 180  
DB 121 POELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAPFFAGTIVTTIGYGNIAPESTEGG 180  
QY 181 KIFCIIYAIIFGPIPLAGIDGDLGTFGKSIARVEKVFRRKQVSTKIRVISTILFI 240  
DB 181 KIFCIIYAIIFGPIPLAGIDGDLGTFGKSIARVEKVFRRKQVSTKIRVISTILFI 240  
QY 241 LAGCIVFVTIPAVIFKYIEGWTALLESYFVVVTLTTVGDFGVAGNAGINREWKPLV 300  
DB 241 LAGCIVFVTIPAVIFKYIEGWTALLESYFVVVTLTTVGDFGVAGNAGINREWKPLV 300  
QY 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKTEEVGEIKAHAAEWKANTVAEPRETRRLSV 360  
DB 301 WFWILVGLAYFAAVLSMIGDMLRVLSKTKTEEVGEIKAHAAEWKANTVAEPRETRRLSV 360  
QY 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
DB 361 EIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINRRP 420  
QY 421 NNRLKGPPEQLNKHGQASDNIINKFGTSRLTKRKNKDLKKTLPEDVQKIYKTRFNY 480  
DB 421 NNRLKGPPEQLNKHGQASDNIINKFGTSRLTKRKNKDLKKTLPEDVQKIYKTRFNY 480  
QY 481 LDEEKEEBETEKMNCNSDNTAMLTDCIQOHAELNGMIPTDTKDREPENNSLLEDRN 538  
DB 481 LDEEKEEBETEKMNCNSDNTAMLTDCIQOHAELNGMIPTDTKDREPENNSLLEDRN 538

RESULT 4  
AAE21804  
ID AAE21804 standard; protein; 543 AA.  
XX  
XX AAE21804;  
XX  
XX 16-JUL-2002 (first entry)  
XX Human TREK2 protein.  
XX  
XX Human; hTREK2 protein; cancer; diabetes; pulmonary disease; asthma;  
XX cardiovascular disease; inflammatory disease; psychiatric disorder;  
XX renal disease; neurodegenerative disease; neurological disorder;  
XX Alzheimer's disease; depression; schizophrenia; stroke; vaccine; trauma;  
XX pain.  
XX Homo sapiens.  
XX  
XX GB2365010-A.  
XX

PD	13-FEB-2002.	Db	498 MCNSDNSSTAMLTDCIQHAELNGMIPDTDKREPENNILLEDRN 543
XX		RESULT 5	
PF	24-APR-2001; 2001GB-00010129.	AAU81354	
XX		ID	AAU81354 standard; protein; 543 AA.
XX	25-APR-2000; 2000GB-00010060.	XX	
PR	01-JUN-2000; 2000GB-00013370.	AC	AAU81354;
XX		XX	
PA	(SMIK ) SMITHKLINE BEECHAM CORP.	DT	09-APR-2002 (first entry)
PA	(SMIK ) SMITHKLINE BEECHAM PLC.	XX	
XX		XX	Novel human ion channel protein #34.
PI	Chapman CG, Duckworth DM;	DE	
XX		XX	
DR	WPI; 2002-332557/37.	KW	Human; ion channel; anti-HIV; analgesic; cytostatic; antidiabetic;
DR	N-PSDB; AAD34451.	KW	anorectic; metabolic; hypertensive; hypotensive; thrombolytic; cardiac;
XX		KW	antithrombotic; neuroleptic; antimigraine; antiparkinsonian;
XX	Novel human TREK2 (HTRK2) polypeptide and polynucleotide encoding it,	KW	tranquiliser; antidepressant; neuroprotective; anticonvulsant; pain;
PT	useful for identifying agonists and antagonists in the treatment of	KW	antiinflammatory; antineumatic; antiarthritic; immunosuppressive;
PT	diseases associated with a HTRK2 imbalance, such as diabetes, cancers or	KW	antipsoriatic; antiasthmatic; vulvar; neurologic disorder; obesity;
PT	asthma.	KW	psychiatric disorder; gene therapy; asthma; traumatic brain injury;
XX		KW	human immunodeficiency virus; HIV-1; HIV-2; cancer; diabetes; anorexia;
PS	Claim 1; Page 21-22; 29pp; English.	KW	myocardial infarction; Parkinson's disease; thyroid disorder; inflammation;
CC	The invention relates to human HTRK2 polypeptides and nucleic acid	KW	dementia; Huntington's disease; thyroid disorder; inflammation;
CC	molecules encoding such polypeptides. TREK2 polypeptides are useful in	KW	autoimmune disorder; hormonal disorder; renal failure; psoriasis;
CC	screening assays to identify compounds that may stimulate or inhibit	XX	
CC	their function or level of expression. Sequences of the invention are	OS	Homo sapiens.
CC	used to treat cancer, diabetes, asthma, pulmonary disease, cardiovascular	XX	
CC	diseases, inflammatory disease, renal disease, pain, psychiatric	PN	WO200185788-A2.
CC	disorders including depression and schizophrenia, neurodegenerative	XX	
CC	disease including Alzheimer's disease, stroke and head trauma and	PD	15-NOV-2001.
CC	neurological disorders. They are also used as vaccines. The present	XX	
CC	sequence is human HTRK2 protein	XX	
XX		PF	10-MAY-2001; 2001WO-US014965.
SQ	Sequence 543 AA;	XX	
		PR	10-MAY-2000; 2000US-0203305P.
	Query Match	PR	23-MAY-2000; 2000US-0206526P.
	Best Local Similarity 97.7%; Score 2697; DB 5; Length 543;	PR	25-MAY-2000; 2000US-0207033P.
	Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR	25-MAY-2000; 2000US-0207092P.
QY	13 VAVPAAAPVCPKATNCGPPAPAPPTPRPISISSRATVVARMEGTSGGGLQTVKWKTV 72	PR	25-MAY-2000; 2000US-0207093P.
Db	18 VAVPAAAPVCPKATNCGPPAPAPPTPRPISISSRATVVARMEGTSGGGLQTVKWKTV 77	PR	07-JUL-2000; 2000US-0216893P.
QY	73 VAFVFWVVVYLVGTGLVFRALQEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132	PR	04-AUG-2000; 2000US-0223245P.
Db	78 VAFVFWVVVYLVGTGLVFRALQEPSSQKNTIALEKAEFLRDHVCVSPQELTILQHAL 137	XX	04-OCT-2000; 2000US-0237873P.
QY	133 DADNAGVSPIGNSSNNSHDLGSAFFAGTVITIGVNIAPSTEGGKIFCILYAIFGI 192	PA	(PHAA ) PHARMACIA & UPJOHN CO.
Db	138 DADNAGVSPIGNSSNNSHDLGSAFFAGTVITIGVNIAPSTEGGKIFCILYAIFGI 197	XX	
QY	193 PLFGFLLAGIDGLTIFGKSIARVEKVRKQVSOQKIRVISTILILAGCIVFTIPA 252	PI	Roberds SL, Benjamin CW, Karnovsky AM, Ruble CL;
Db	198 PLFGFLLAGIDGLTIFGKSIARVEKVRKQVSOQKIRVISTILILAGCIVFTIPA 257	DR	WPI; 2002-062237/08.
QY	253 VIFKYIEGWTALESIYFVVVTLTVGDFVAGNAGINREWKPLVFWILVGLAYFA 312	XX	N-PSDB; ABK27503.
Db	258 VIFKYIEGWTALESIYFVVVTLTVGDFVAGNAGINREWKPLVFWILVGLAYFA 317	XX	
QY	313 AVLSMIGDWLRVLKSTKEEVEGETKAHAAEKANTVAFRETRRLRSLVEIHDKLOAATI 372	PT	New polynucleotides, useful for identifying ion channel activity
Db	318 AVLSMIGDWLRVLKSTKEEVEGETKAHAAEKANTVAFRETRRLRSLVEIHDKLOAATI 377	PT	modulators that are used for treating Parkinson's disease, schizophrenia,
QY	373 RSMERRRLGLDQRAHSLDMSPEKRSVFAALDTGRFKASQESINRPNRLKGPQLN 432	PT	migraine, anxiety, manic depression, encodes the ion channel polypeptide.
Db	378 RSMERRRLGLDQRAHSLDMSPEKRSVFAALDTGRFKASQESINRPNRLKGPQLN 437	PS	Claim 2; Page 89; 172pp; English.
QY	433 KHGQASDNTINFGSTSRUTKRNKDLKTLPEDEVOKYKTPRNTSLDEEKKBEETEX 492	CC	The invention relates to an isolated nucleic acid molecule (I) which
Db	438 KHGQASDNTINFGSTSRUTKRNKDLKTLPEDEVOKYKTPRNTSLDEEKKBEETEX 497	CC	encodes a novel ion channel protein, ion-x (II). The nucleic acid,
QY	493 MCNSDNSSTAMLTDCIQHAELNGMIPDTDKREPENNILLEDRN 538	CC	protein and antibody are useful for identifying a compound which binds a
		CC	nucleic acid molecule encoding ion-x. These are useful for treatment of a
		CC	neurological or psychiatric disorder which modulates ligand binding to
		CC	ion-x in neurons of the mammal; in gene therapy to restore ion-x activity
		CC	in certain disease states; for treating asthma, traumatic brain injury,
		CC	etc; modulators of ion-x activity or expression are useful for treating
		CC	diseases such as viral infections caused by human immunodeficiency virus
		CC	(HIV)-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia,
		CC	hypotension, hypertension, thrombosis, myocardial infarction,
		CC	cardiomyopathies, atherosclerosis, Parkinson's disease, schizophrenia,
		CC	migraine, anxiety, manic depression, dementia, Huntington's disease,
		CC	thyroid disorders, inflammatory conditions, rheumatoid arthritis,
		CC	autoimmune disorders, hormonal disorders, renal failure, psoriasis, and
		CC	movement disorders. AAU81321-AAU81360 represent human ion channel protein
		CC	sequences of the invention

XX	Sequence 543 AA;	
XX	Query Match	97.7%; Score 2697; DB 5; Length 543;
XX	Best Local Similarity	100.0%; Pred. No. 3.6e-238; Indels 0; Gaps 0;
XX	Matches 526; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	13 VAVPAAAPVCPKSAATNGQPPAPAPTPTPLSLSSSRATVVARMEGTSQGLQTVMKWKT 72	
DB	18 VAVPAAAPVCPKSAATNGQPPAPAPTPTPLSLSSSRATVVARMEGTSQGLQTVMKWKT 77	
QY	73 VAIFVWVYVLTGGLVFRALFQPESSQKNTALEKAEFLRDHVCVSPQLETLIOHAL 132	
DB	78 VAIFVWVYVLTGGLVFRALFQPESSQKNTALEKAEFLRDHVCVSPQLETLIOHAL 137	
QY	133 DADNAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTCYGNIAPISTEGGKIFCILYAI 192	
DB	138 DADNAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTCYGNIAPISTEGGKIFCILYAI 197	
QY	193 PLFGFLLAGIGDQGTIFGKSIARVEKVRKKQVSTKIRVISTILFILAGCIVFTIPA 252	
DB	198 PLFGFLLAGIGDQGTIFGKSIARVEKVRKKQVSTKIRVISTILFILAGCIVFTIPA 257	
QY	253 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 312	
DB	258 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 317	
QY	313 AVLISMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 372	
DB	318 AVLISMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 377	
QY	373 RSMERRELGLDQRAHSLDMLSPKRSVFALDTGRFKASSQESINRNPNRLKGPQLN 432	
DB	378 RSMERRELGLDQRAHSLDMLSPKRSVFALDTGRFKASSQESINRNPNRLKGPQLN 437	
QY	433 KHGGGASEDNIINFGSTSLTKRKNKDLKXTLPEDVQKIYKTFRNYSLDEEKEETEK 492	
DB	438 KHGGGASEDNIINFGSTSLTKRKNKDLKXTLPEDVQKIYKTFRNYSLDEEKEETEK 497	
QY	493 MCNSDNSSTAMLTDCIQHAELNGMIPPTDKREPNNSLLDRN 538	
DB	498 MCNSDNSSTAMLTDCIQHAELNGMIPPTDKREPNNSLLDRN 543	

RESULT 6

AAU79472	
ID	AAU79472 standard; protein; 543 AA.
XX	AAU79472;
XX	15-JUL-2002 (first entry)
DE	Human novel transporter protein.
XX	Human; transporter; transgenic; transporter mediated disease;
KW	drug screening; pharmacogenomic analysis; chromosome 18.
XX	Homo sapiens.
XX	W0200224748-A2.
XX	28-MAR-2002.
XX	19-SEP-2001; 2001WO-US029211.
XX	19-SEP-2000; 2000US-0233663P.
PR	06-DEC-2000; 2000US-00729920.
XX	(PEKE ) PE CORP NY.
PA	Guegler K, Ketchum KA, Di Francesco V, Beasley EM;
XX	WPI; 2002-351995/38.

DR	N-PSDB; ABK49585, ABK49586.	
XX	New human transporter proteins and nucleic acids, useful as models in the	
PT	development of human therapeutic agents, in identifying therapeutic	
PT	proteins, or as query sequence in database searches to identify related	
PT	sequences.	
XX	Claim 1; Fig 2; 207pp; English.	
PS	The invention relates to a new isolated peptide being a human transporter	
XX	protein, an allelic variant, orthologue, fragment or sequence that is 70%	
CC	homologous to the transporter. Also included are a nucleic acid encoding	
CC	the transporter (including allelic variants, orthologue, fragment or	
CC	complement), an antibody against the protein, a gene chip comprising the	
CC	nucleic acids, a transgenic non-human animal comprising the nucleic	
CC	acids, a nucleic acid vector comprising the nucleic acids, a host cell	
CC	containing the vector, identifying agents that bind to and/or modulate	
CC	the function of the transporter, and treating a disease or condition	
CC	mediated by a human transporter protein by administering to the patient	
CC	an identified agent or modulator. The peptide sequences and the nucleic	
CC	acid sequences encoding these peptides can be used as models for the	
CC	development of human therapeutic targets, aid in the identification of	
CC	therapeutic proteins, and serve as targets for the development of human	
CC	therapeutic agents that modulate transporter activity in cells and	
CC	tissues that express the transporter. These sequences may also be used as	
CC	query sequence in database searches to identify other family members or	
CC	related sequences. The proteins may be used to raise antibodies or to	
CC	elicit immune response; as a reagent in assays designed to quantitatively	
CC	determine protein levels in biological fluids; as markers for tissues in	
CC	which the corresponding protein is expressed; in drug screening assays in	
CC	cell-based or cell-free systems; to identify compounds that modulate	
CC	transporter activity of the protein in its natural state or altered form	
CC	that causes a specific disease or pathology associated with the	
CC	transporter; as a target for diagnosing a disease or predisposition to	
CC	disease mediated by the peptide; and in pharmacogenomic analysis. The	
CC	nucleic acids are useful as hybridisation probes or primers; in	
CC	monitoring the effectiveness of modulating compounds on the expression or	
CC	activity of the transporter gene in clinical trials or treatment regimen;	
CC	in diagnostic assays for qualitative changes in transporter nucleic acid	
CC	expression; and as antisense constructs. The gene for the transporter is	
CC	located on chromosome 18. The present sequence represents the novel human	
CC	transporter	
XX	Sequence 543 AA;	
QY	Query Match	97.7%; Score 2697; DB 5; Length 543;
DB	Best Local Similarity	100.0%; Pred. No. 3.6e-238; Indels 0; Gaps 0;
DB	Matches 526; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	13 VAVPAAAPVCPKSAATNGQPPAPAPTPTPLSLSSSRATVVARMEGTSQGLQTVMKWKT 72	
DB	18 VAVPAAAPVCPKSAATNGQPPAPAPTPTPLSLSSSRATVVARMEGTSQGLQTVMKWKT 77	
QY	73 VAIFVWVYVLTGGLVFRALFQPESSQKNTALEKAEFLRDHVCVSPQLETLIOHAL 132	
DB	78 VAIFVWVYVLTGGLVFRALFQPESSQKNTALEKAEFLRDHVCVSPQLETLIOHAL 137	
QY	133 DADNAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTCYGNIAPISTEGGKIFCILYAI 192	
DB	138 DADNAGVSPICGNSSNNSHWDLGSAFFAGTAVTTTCYGNIAPISTEGGKIFCILYAI 197	
QY	193 PLFGFLLAGIGDQGTIFGKSIARVEKVRKKQVSTKIRVISTILFILAGCIVFTIPA 252	
DB	198 PLFGFLLAGIGDQGTIFGKSIARVEKVRKKQVSTKIRVISTILFILAGCIVFTIPA 257	
QY	253 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 312	
DB	258 VIFKYIEGWTALSIYFVVVTLTTVGDFVAGNAGINREWKPLVFWFVILVGLAYFA 317	
QY	313 AVLISMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 372	
DB	318 AVLISMIGDWLRVLSKTKKEVGEIKAHAAEWKANVTAEFRTRRLRSVEIHDKLQRAATI 377	

QY 373 RSMERRRLGLDORAHSLDMLSPKESVFAALDTGRFKASSOESINNRPNLRLKGPQLN 432  
 DB 378 RSMERRRLGLDORAHSLDMLSPKESVFAALDTGRFKASSOESINNRPNLRLKGPQLN 437  
 QY 433 KHGOQASEDNIIKFGSTSRITKRNKDLKTLDPEDVQKIYKTFRNYSLDDEKKEEETEK 492  
 DB 438 KHGOQASEDNIIKFGSTSRITKRNKDLKTLDPEDVQKIYKTFRNYSLDDEKKEEETEK 497  
 QY 493 MCNSDNSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538  
 DB 498 MCNSDNSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543

RESULT 7  
 ID ABB83542  
 AC ABB83542  
 XX  
 DT 24-SEP-2002 (first entry)  
 DE Hypothalamus-expressed potassium channel protein.  
 KW Hypothalamus; potassium channel; obesity; human.  
 OS Homo sapiens.  
 XX  
 PN WO200252000-A1.  
 PD 04-JUL-2002;  
 XX  
 PF 25-DEC-2001; 2001WO-JP011330.  
 PR 26-DEC-2000; 2000JP-00996020.  
 XX  
 PA (YAMA) YAMANOUCHI PHARM CO LTD.  
 PI Yokoi H, Inamura K, Sano Y, Miyake A, Mochizuki S;  
 XX  
 DR WPI; 2002-508889/54.  
 N-PSDB; ABN85879.  
 XX  
 PT Hypothalamus-expressed potassium channel protein and encoded  
 PT polynucleotide, applicable in screening inhibitors as anti-obestic agents  
 PT to control food intake and enhanced energy consumption.  
 XX  
 PS Claim 1; Page 39-41; 45pp; Japanese.  
 XX  
 CC This invention relates to a hypothalamus-expressed protein having  
 CC potassium channel activity. The protein and polynucleotide are applicable  
 CC in screening inhibitors as anti-obesity agents to control food intake and  
 CC enhanced energy consumption. The said screening process is advantageous  
 CC as it is convenient to operate. This sequence represents a potassium  
 CC channel activity protein  
 XX  
 SQ Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 5; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-238;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKFSATNQPPAPAPTPTPLRSLSSRATVVARMEGTSGGLQTVMKWKT 72  
 DB 18 VAVPAAAPVCPKFSATNQPPAPAPTPTPLRSLSSRATVVARMEGTSGGLQTVMKWKT 77  
 QY 73 VAI FVVVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLEFLIQHAL 132  
 DB 78 VAI FVVVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLEFLIQHAL 137  
 QY 133 DADNAGVSPIGNSSNNSSHWDLSAFTFAGTVITIGYGNIAPISTEGGKIFCILYAI FGI 192  
 DB 138 DADNAGVSPIGNSSNNSSHWDLSAFTFAGTVITIGYGNIAPISTEGGKIFCILYAI FGI 197

QY 193 PLFGFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIPA 252  
 DB 198 PLFGFLLAGIGDQGLTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIPA 257  
 QY 253 VIFPKYIEGTALLESYFVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLEFLIQHAL 312  
 DB 258 VIFPKYIEGTALLESYFVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQLEFLIQHAL 317  
 QY 313 AVLISMGDLRLVLSKKTKEEVEGEIKAHAAEWKANTVTAFFRETRRRLSVIEIHDKLQRAATI 372  
 DB 318 AVLISMGDLRLVLSKKTKEEVEGEIKAHAAEWKANTVTAFFRETRRRLSVIEIHDKLQRAATI 377  
 QY 373 RSMERRRLGLDORAHSLDMLSPKESVFAALDTGRFKASSOESINNRPNLRLKGPQLN 432  
 DB 378 RSMERRRLGLDORAHSLDMLSPKESVFAALDTGRFKASSOESINNRPNLRLKGPQLN 437  
 QY 433 KHGOQASEDNIIKFGSTSRITKRNKDLKTLDPEDVQKIYKTFRNYSLDDEKKEEETEK 492  
 DB 438 KHGOQASEDNIIKFGSTSRITKRNKDLKTLDPEDVQKIYKTFRNYSLDDEKKEEETEK 497  
 QY 493 MCNSDNSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 538  
 DB 498 MCNSDNSSTAMLTDCIQHAELENGMIPTDTKDRPENNSLLEDNRN 543

RESULT 8  
 ADA05746  
 ID ADA05746 standard; protein; 543 AA.  
 XX  
 AC ADA05746;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX  
 DE Human NOV19a protein SEQ ID NO:106.  
 XX  
 KW human; NOVX; antidiabetic; anorectic; antibacterial; virucide;  
 KW immunomodulator; cytostatic; nootropic; neuroprotective;  
 KW antiparkinsonian; antilipaeamic; gene therapy; human disease;  
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;  
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;  
 KW immune disorder; haematopoietic disorder; dyslipidaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003029424-A2.  
 XX  
 PD 10-APR-2003.  
 XX  
 PF 02-OCT-2002; 2002WO-US031373.  
 XX  
 PR 02-OCT-2001; 2001US-0326483P.  
 PR 05-OCT-2001; 2001US-0327435P.  
 PR 05-OCT-2001; 2001US-0327449P.  
 PR 09-OCT-2001; 2001US-0327517P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328044P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328849P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330143P.  
 PR 18-OCT-2001; 2001US-0330309P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-033266P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 17-APR-2002; 2002US-0373260P.  
 PR 19-APR-2002; 2002US-0373815P.  
 PR 19-APR-2002; 2002US-0373817P.  
 PR 19-APR-2002; 2002US-0373884P.  
 PR 22-APR-2002; 2002US-0374977P.  
 PR 16-MAY-2002; 2002US-0381037P.

Db	78	VAIFVVVVVVVLTGGLVFRALAEQFPSSQKNTTALKAEPFLRHVVCVQSELTLLQHAL	137
Qy	133	DADNAGVSPIGNSNSSSHWDLGSAFFPAGTIVTTTGYGNIAPSTEGGKIFCILYAIFGI	192
Db	138	DADNAGVSPIGNSNSSSHWDLGSAFFPAGTIVTTTGYGNIAPSTEGGKIFCILYAIFGI	197
Qy	193	PLFGELLAGIDQLGTIFGKSIAKVEKPKKQVSKTKIRVISTILFILAGCIVFTTIA	252
Db	198	PLFGELLAGIDQLGTIFGKSIAKVEKPKKQVSKTKIRVISTILFILAGCIVFTTIA	257
Qy	253	VFFKIEGWTALESIFYVVTTLTTVGFGDFVAGNAGINRYREWKPLVWFVILVGLAYFA	312
Db	258	VFFKIEGWTALESIFYVVTTLTTVGFGDFVAGNAGINRYREWKPLVWFVILVGLAYFA	317
Qy	313	AVLSMIGDWLRVLSKTKKEEVGEIKAHAAEWKANVTAEPRETRRRLSVEIHDKLQRAANI	372
Db	318	AVLSMIGDWLRVLSKTKKEEVGEIKAHAAEWKANVTAEPRETRRRLSVEIHDKLQRAANI	377
Qy	373	RSMERRRRLGLDORAHSLDMLSPKRSVPAALDTGRFKASSQESINNRPNRLKGPQLN	432
Db	378	RSMERRRRLGLDORAHSLDMLSPKRSVPAALDTGRFKASSQESINNRPNRLKGPQLN	437
Qy	433	KHGQASEDNIINFGSTSRLTTRKKNLDLKTLPEDVQKIYKTRFNYSLDEEKKEBETEK	492
Db	438	KHGQASEDNIINFGSTSRLTTRKKNLDLKTLPEDVQKIYKTRFNYSLDEEKKEBETEK	497
Qy	493	MCNSDNSSTAMLTDCICQHAELNGMPTDTDKOREPENNLSLLEDRN	538
Db	498	MCNSDNSSTAMLTDCICQHAELNGMPTDTDKOREPENNLSLLEDRN	543
RESULT 9			
ADE08315			
ID	ADE08315 standard; protein; 543 AA.		
XX	ADE08315;		
XX	29-JAN-2004 (first entry)		
XX	Novel protein (useful for identifying genetic disorders) #470.		
DE	novel gene; novel protein; tissue marker; molecular weight marker;		
XX	chromosome marker; genetic disorder.		
XX	Unidentified.		
OS	WO2003054152-A2.		
PN	03-JUL-2003.		
PD	10-DEC-2002; 2002WO-US39555.		
XX	10-DEC-2001; 2001US-0339739P.		
PR	11-DEC-2001; 2001US-0339453P.		
PR	14-MAR-2002; 2002US-0385031P.		
PR	14-MAR-2002; 2002US-0385384P.		
PR	12-APR-2002; 2002US-0372381P.		
PR	12-APR-2002; 2002US-0372615P.		
PR	22-APR-2002; 2002US-00128558.		
PR	24-APR-2002; 2002US-0376045P.		
XX	(HYSE-) HYSEQ INC.		
PA	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;		
XX	Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;		
PI	Ma Y, Wang D, Chen R, Xu C, Boyle BJ;		
PI	WPI: 2003-569235/53.		
DR	N-PSDB; ADE07404.		
XX	New polynucleotides, useful for expressing recombinant proteins for		
PT	analysis, characterization or therapeutic use, or as markers for tissues		

PT in which the corresponding protein is preferentially expressed.

XX Claim 20; SEQ ID NO 1381; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel  
 CC proteins. The DNA and protein sequences of the invention are useful as:  
 CC markers for tissues in which the corresponding protein is preferentially  
 CC expressed; as molecular weight markers on gels; as chromosome markers or  
 CC tags; to identify chromosomes or to map related gene positions; and to  
 CC compare with endogenous DNA sequences in patients to identify potential  
 CC genetic disorders. The present amino acid sequence represents a protein  
 CC of the invention.

XX Sequence 543 AA;

Query Match 97.7%; Score 2697; DB 7; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-238;  
 Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	13	VAVPAAAPVCPKSAATNGQPAPAPPTPTPLRISISSRATVVARMEGTSOGGLQTVNWKTV	72
Db	18	VAVPAAAPVCPKSAATNGQPAPAPPTPTPLRISISSRATVVARMEGTSOGGLQTVNWKTV	77
QY	73	VAFVFWVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIQHAL	132
Db	78	VAFVFWVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIQHAL	137
QY	133	DADNAGVSPIGNSSNNSHWDLSGAFPAFTVITIGVNTAPSTEGKIFCILYALPGI	192
Db	138	DADNAGVSPIGNSSNNSHWDLSGAFPAFTVITIGVNTAPSTEGKIFCILYALPGI	197
QY	193	PLFGFLLAGIGDQGTIFGKSIARVEKVRKQVSTQKIRVISTILFILAGCIVFTIPA	252
Db	198	PLFGFLLAGIGDQGTIFGKSIARVEKVRKQVSTQKIRVISTILFILAGCIVFTIPA	257
QY	253	VIFKPIEGWTALESIFVFWVLTITVGFQDFVAGNAGINREWKPLVFWWILGLAYFA	312
Db	258	VIFKPIEGWTALESIFVFWVLTITVGFQDFVAGNAGINREWKPLVFWWILGLAYFA	317
QY	313	AVLSMIGDLVLSKTKKEEYGEIKAHAAEWKANVTAEFTRRLRSVEIHDKLRQANTI	372
Db	318	AVLSMIGDLVLSKTKKEEYGEIKAHAAEWKANVTAEFTRRLRSVEIHDKLRQANTI	377
QY	373	RSMEERRGLDQRAHSLDMLSPKRSVPAALDTGRFKASSOESINNRPNRLKGPQLN	432
Db	378	RSMEERRGLDQRAHSLDMLSPKRSVPAALDTGRFKASSOESINNRPNRLKGPQLN	437
QY	433	KHGQASDNIINKGTSRLTKRKNKDLKTLPEVDQKIYKTPRNSLDEEKEETEX	492
Db	438	KHGQASDNIINKGTSRLTKRKNKDLKTLPEVDQKIYKTPRNSLDEEKEETEX	497
QY	493	MCNSDNSSTAMLTDCIQHAELNGMIPTDTKDRPENNSLLEDRN	538
Db	498	MCNSDNSSTAMLTDCIQHAELNGMIPTDTKDRPENNSLLEDRN	543

RESULT 10  
 AAU79473  
 ID AAU79473 standard; protein; 543 AA.

XX AAU79473;

XX 15-JUL-2002 (first entry)

XX Human novel transporter protein variant.

XX Human; transporter; transgenic; transporter mediated disease;  
 KW drug screening; pharmacogenomic analysis; chromosome 18.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 233

/note= "wild-type Gln substituted by Lys"

XX WO200224748-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-US029211.

XX 19-SEP-2000; 2000US-0233663P.

XX 06-DEC-2000; 2000US-00729920.

XX (PEKE ) PE CORP NY.

XX Guegler K, Ketchum KA, Di Francesco V, Beasley EM;

XX WPI; 2002-351999/38.

XX New human transporter proteins and nucleic acids, useful as models in the  
 PT development of human therapeutic agents, in identifying therapeutic  
 PT proteins, or as query sequence in database searches to identify related  
 PT sequences.

XX Disclosure; Page; 207pp; English.

XX The invention relates to a new isolated peptide being a human transporter  
 CC protein, an allelic variant, orthologue, fragment or sequence that is 70%  
 CC homologous to the transporter. Also included are a nucleic acid encoding  
 CC the transporter (including allelic variants, orthologue, fragment or  
 CC complement), an antibody against the protein, a gene chip comprising the  
 CC nucleic acids, a transgenic non-human animal comprising the nucleic  
 CC acids, a nucleic acid vector comprising the nucleic acids, a host cell  
 CC containing the vector, identifying agents that bind to and/or modulate  
 CC the function of the transporter, and treating a disease or condition  
 CC mediated by a human transporter protein by administering to the patient  
 CC an identified agent or modulator. The peptide sequences and the nucleic  
 CC acid sequences encoding these peptides can be used as models for the  
 CC development of human therapeutic targets, aid in the identification of  
 CC therapeutic proteins, and serve as targets for the development of human  
 CC tissues that express the transporter. These sequences may also be used as  
 CC queries that express the transporter. The proteins may be used to raise antibodies or  
 CC related sequences. The proteins may be used to raise antibodies or to  
 CC elicit immune responses; as a reagent in assays designed to quantitatively  
 CC determine protein levels in biological fluids; as markers for tissues in  
 CC which the corresponding protein is expressed; in drug screening assays in  
 CC cell-based or cell-free systems; to identify compounds that modulate  
 CC transporter activity of the protein in its natural state or altered form  
 CC that causes a specific disease or pathology associated with the  
 CC transporter; as target for diagnosing a disease or predisposition to  
 CC disease mediated by the peptide, and in pharmacogenomic analysis. The  
 CC nucleic acids are useful as hybridisation probes or primers; in  
 CC monitoring the effectiveness of modulating compounds on the expression or  
 CC activity of the transporter gene in clinical trials or treatment regimen;  
 CC in diagnostic assays for qualitative changes in transporter nucleic acid  
 CC expression; and as antisense constructs. The gene for the transporter is  
 CC located on chromosome 18. The present sequence represents a variant of  
 CC the novel human transporter. Note: The present sequence is not shown in  
 CC the specification but was created by the indexer from the information in  
 CC figure 3 and the transporter sequence appearing as AAU79472

XX Sequence 543 AA;

Query Match 97.6%; Score 2693; DB 5; Length 543;

Best Local Similarity 99.8%; Pred. No. 8.5e-238;

Matches 525; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 VAVPAAAPVCPKSAATNGQPAPAPPTPTPLRISISSRATVVARMEGTSOGGLQTVNWKTV 72

Db 18 VAVPAAAPVCPKSAATNGQPAPAPPTPTPLRISISSRATVVARMEGTSOGGLQTVNWKTV 77

QY 73 VAFVFWVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIQHAL 132

Db 78 VAFVFWVVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHVCVSPQELTIQHAL 137



QY 133 DADNAGVSPIGNSSNNSHMDLGSAPFFAGFVITITIGYGNIAPISTEGGKIFCILYAFGI 192  
 DB 138 DADNAGVSPIGNSSNNSHMDLGSAPFFAGFVITITIGYGNIAPISTEGGKIFCILYAFGI 197  
 QY 193 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSOQKIRVISTILFILAGCIVFTIPA 252  
 DB 198 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSOQKIRVISTILFILAGCIVFTIPA 257  
 QY 253 VIFKYIEGWTALSIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVILVGLAYFA 312  
 DB 258 VIFKYIEGWTALSIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVILVGLAYFA 317  
 QY 313 AVLSMIGDWRVLVSKTKKEVGEIKAHAAEWKANVTAEFTRRRRLSVEIHDKLQAAFI 372  
 DB 318 AVLSMIGDWRVLVSKTKKEVGEIKAHAAEWKANVTAEFTRRRRLSVEIHDKLQAAFI 377  
 QY 373 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNNRPNRLKGPQLN 432  
 DB 378 RSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNNRPNRLKGPQLN 437  
 QY 433 KHGGGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEBETEK 492  
 DB 438 KHGGGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEBETEK 497  
 QY 493 MCNSDNSSTAMLTDCIQOHAELNGMIPDTDKREPENNSLLEDNRN 538  
 DB 498 MCNSDNSSTAMLTDCIQOHAELNGMIPDTDKREPENNSLLEDNRN 543  
 RESULT 11  
 AAO14193  
 ID AAO14193 standard; protein; 724 AA.  
 AC AAO14193;  
 XX  
 DT 03-MAY-2002 (first entry)  
 XX  
 DE Human transporter and ion channel TRICH-10.  
 XX  
 XX Human; transporter and ion channel; TRICH; transport disorder;  
 XX neurological disorder; muscle disorder; immunological disorder;  
 KW cell proliferative disorder; neuroprotective; nontropic;  
 KW cerebroprotective; immunosuppressive; cytostatic; respiratory; muscular;  
 KW gene therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200204520-A2.  
 PN  
 XX 17-JAN-2002.  
 XX  
 XX 05-JUL-2001; 2001WO-US021448.  
 XX  
 XX 07-JUL-2000; 2000US-0216547P.  
 PR 14-JUL-2000; 2000US-0218232P.  
 PR 21-JUL-2000; 2000US-0220112P.  
 PR 28-JUL-2000; 2000US-0221839P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;  
 PI Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;  
 PI Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;  
 PI Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal P;  
 PI Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;  
 PI Kearney L, Thangavelu K, Das D, Pollicky JL;  
 XX WPI; 2002-205969/26.  
 DR N-PSDB; AAL44676.  
 DR  
 XX New human transporters and ion channel polypeptides for diagnosing,  
 PT treating or preventing transport, neurological, muscle, immunological and

PT cell proliferative disorders.

XX Claim 1; Page 158-160; 230pp; English.

XX The present invention provides the protein and coding sequences of a  
 CC number of human transporter and ion channel proteins, designated TRICH-1-  
 CC TRICH-32. The sequences can be used in the treatment of transport, the  
 CC neurological, muscle, immunological and cell proliferative disorders. The  
 CC present sequence is a protein of the invention

XX Sequence 724 AA;

Query Match 96.3%; Score 2657.5; DB 5; Length 724;

Best Local Similarity 98.7%; Pred. No. 2.3e-234; Indels 5; Gaps 2;

Matches 523; Conservative 1; Mismatches 1; Indels 5; Gaps 2;

QY 13 VAVPAAAPVPCOPKSNATNGQPAPAPPTPRLSISSRATVVARMEGTSOGGLQTVMKWTV 72

DB 196 VAVPAAAPVPCOPKSNATNGQPAPAPPTPRLSISSRATVVARMEGTSOGGLQTVMKWTV 255

QY 73 VAFVWVYLVGTGLVFRALDQPPESQKNTIALEKAEFLRDHVCVSPQELTILQHAL 132

DB 256 VAFVWVYLVGTGLVFRALDQPPESQKNTIALEKAEFLRDHVCVSPQELTILQHAL 315

QY 133 DADNAGVSPIGNSSNNSHMDLGSAPFFAGFVITITIGYGNIAPISTEGGKIFCILYAFGI 192

DB 316 DADNAGVSPIGNSSNNSHMDLGSAPFFAGFVITITIGYGNIAPISTEGGKIFCILYAFGI 374

QY 193 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSOQKIRVISTILFILAGCIVFTIPA 252

DB 375 PLFGFLAGIGDQGTIFGKSIARVEKVRKQVSOQKIRVISTILFILAGCIVFTIPA 434

QY 253 VIFKYIEGWTALSIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVILVGL 308

DB 435 VIFKYIEGWTALSIYFVVVTLTTVGFDFVAGNAGINREWKPLVFWFVILVGL 494

QY 309 AYFAAVLSMIGDWRVLVSKTKKEVGEIKAHAAEWKANVTAEFTRRRRLSVEIHDKLQ 368

DB 495 AYFAAVLSMIGDWRVLVSKTKKEVGEIKAHAAEWKANVTAEFTRRRRLSVEIHDKLQ 554

QY 369 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNNRPNRLKGP 428

DB 555 AATIRSMERRRLGLDQRAHSLDMLSPKRSVFAALDTGRFKASSQESINNNRPNRLKGP 614

QY 429 EQLNKHGGGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE 488

DB 615 EQLNKHGGGASEDNIINKFGSTSLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE 674

QY 489 ETEKYCNSDNSSTAMLTDCIQOHAELNGMIPDTDKREPENNSLLEDNRN 538

DB 675 ETEKYCNSDNSSTAMLTDCIQOHAELNGMIPDTDKREPENNSLLEDNRN 724

RESULT 12

ABG02731

ID ABG02731 standard; protein; 383 AA.

XX AC ABG02731;

XX 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #2722.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

PF

XX 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX (HYSE-) HYSEQ INC.  
XX Drmanac RT, Liu C, Tang YT;  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS66918.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 20; SEQ ID NO 33090; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 383 AA;  
Query Match 59.1%; Score 1630; DB 4; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1.7e-140;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 222 RKQVSTQKIRVISITLILAGCIVFVTPAVIFKYIEGWTALSIYFVVVTLTTVGFSD 281  
DB 67 RKQVSTQKIRVISITLILAGCIVFVTPAVIFKYIEGWTALSIYFVVVTLTTVGFSD 126  
QY 282 FVAGNAGINREWKYPLVFWILVGLAYFAAVALSMIGDWLRVLSKTTKEVGIKAHAA 341  
DB 127 FVAGNAGINREWKYPLVFWILVGLAYFAAVALSMIGDWLRVLSKTTKEVGIKAHAA 186  
QY 342 EKANVTAFRETRRLSVEIHDKLQRAATRSWERRLGLDQRAHSLDMLSPKRSVEA 401  
DB 187 EKANVTAFRETRRLSVEIHDKLQRAATRSWERRLGLDQRAHSLDMLSPKRSVEA 246  
QY 402 ALDTCGRFKASSQESINNRPNRLRKGPPQLNKGQASDNIINKFGSTSLTRKKNKDL 461  
DB 247 ALDTCGRFKASSQESINNRPNRLRKGPPQLNKGQASDNIINKFGSTSLTRKKNKDL 306  
QY 462 KKTLPEDVQKIYKTRNYSLEDEKKEETKWCNCSDNSSTAMLTDCIQCHAELENGMIPT 521  
DB 307 KKTLPEDVQKIYKTRNYSLEDEKKEETKWCNCSDNSSTAMLTDCIQCHAELENGMIPT 366  
QY 522 DTKDREPENNSLLEDNRN 538  
DB 367 DTKDREPENNSLLEDNRN 383  
RESULT 13  
ABG08305

ID  
XX ABG08305 standard; protein; 557 AA.  
AC ABG08305;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE Novel human diagnostic protein #8296.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
XX WPI; 2001-639362/73.  
DR N-PSDB; AAS72492.  
XX  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 20; SEQ ID NO 38664; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 557 AA;  
Query Match 51.2%; Score 1412.5; DB 4; Length 557;  
Best Local Similarity 72.4%; Pred. No. 2.6e-120;  
Matches 297; Conservative 2; Mismatches 18; Indels 93; Gaps 4;  
QY 222 RKQVSTQKIRVISITLILAGCIVFVTPAVIFKYIEGWTALSIYFVVVTLTTVGFSD 281  
DB 148 RKQVSTQKIRVISITLILAGCIVFVTPAVIFKYIEGWTALSIYFVVVTLTTVGFSD 207  
QY 282 FVAGNAGINREWKYPLVFWILVGLAYFAAVALSMIGDWLRVLSKTTKEVGIKAHAA 341  
DB 208 FVAGNAGINREWKYPLVFWILVGLAYFAAVALSMIGDWLRVLSKTTKEVGIKAHAA 267  
QY 306 FVAGNAGINREWKYPLVFWILVGLAYFAAVALSMIGDWLRVLSKTTKEVGIKAHAA 330

Db 268 LMQERVVXKEPKAAAPNREGLGTEKLEFXRXEVAAPHAVALSMIGDMLRVLSKTK 327  
QY 331 EE-----VGEIKAAAEKAWKANTVAETFRTRRLSVIEHDKLOR 368  
Db 328 EECVRPLFKSPFNRLGLGVAHHVGEIKAAAEKAWKANTVAETFRTRRLSVIEHDKLOR 387  
QY 369 AATIRSMERRRLGIDQRAHSLDMLSPKRSVFAALDTGRPKASSQSSINNRPNNLKGP 428  
Db 388 AATIRSMERRRLGIDQRAHSLDMLSPKRSVFAALDTGRPKASSQSSINNRPNNLKGP 447  
QY 429 EQLNKGQGSASEDNIINKFGSTGRRLTKRKNKDLKKTLPEDVQKIYKTFRNSLDEKKEE 488  
Db 448 EQLNKGQGSASEDNIINKFGSTGRRLTKRKNKDLKKTLPEDVQKIYKTFRNSLDEKKEE 507  
QY 489 ETEKNCNSDSSAMLTDCIQQAELNEMIPDTKDRPENNSLLEDRN 538  
Db 508 ETEKNCNSDSSAMLTDCIQQAELNEMIPDTKDRPENNSLLEDRN 557

RESULT 14  
AAE10342  
ID AAE10342 standard; protein; 411 AA.  
AC AAE10342;  
DT 10-DEC-2001 (first entry)  
DE Murine TREK-1 potassium channel protein.  
KW Marine; potassium channel protein; TREK-1; anaesthetic; analgesia;  
KW amnesia.  
OS Mus musculus.  
PN WO200047738-A2.  
PD 17-AUG-2000.  
PF 11-FEB-2000; 2000WO-IB000226.  
PR 12-FEB-1999; 99US-0119727P.  
PR 11-FEB-2000; 2000US-00503089.  
XX (CNRS ) CNRS CENT NAT RECH SCI.  
XX Lazdunski M, Honore E, Lesage F, Roney G, Patel AJ;  
XX WPI; 2000-549146/50.  
XX N-PSDB; AAD17497.  
XX Novel nucleic acid encoding a TREK-1 potassium channel protein for  
PT transfecting cells to be used to identify compounds with anesthetic  
PT properties.  
XX Claim 9; Page 32-33; 39pp; English.  
XX The invention relates to human and mouse TREK-1 potassium channel  
CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is  
CC useful for transfecting cells to induce expression of the TREK-1  
CC potassium channel protein. These cells are then used in assays to  
CC identify compounds which have anaesthetic properties, producing a safe,  
CC reversible state of unconsciousness with concurrent amnesia and analgesia  
CC in a mammal upon inhalation. The present sequence is murine TREK-1  
CC potassium channel protein  
XX Sequence 411 AA;  
SQ Query Match 45.3%; Score 1251.5; DB 3; Length 411;  
Best Local Similarity 64.3%; Pred. No. 9.7e-106;  
Matches 24; Conservative 54; Mismatches 66; Indels 17; Gaps 5;  
QY 17 AAAPVQPKSATNGQPAPAPTPTPLRLSSSRATVVA-RWEGTSQGLQTVMKWKTVAI 75

Db 2 AAPDLDPKSA-----AQNSKPRLSFSKPTVLASRVESDS---AINMKWKTVSTI 50  
QY 76 FVWVWVYLVLTGGLVFRALQEPFSSQKNTIALEKAEFLRDHVCVSPQEFLETLIQHALDAD 135  
Db 51 FLVWVLYLIIGAAVFKALEQPEISQRTTIVIQOTFIAQHACVNSTELDELICQIVAAI 110  
QY 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTVITTTIGVNIAPSTEGGKIFCIIYAFIGPLF 195  
Db 111 NAGIIPLCNSSNQVSHWDLGSSFFAGTVITTTIGFNIISPRTEGKIFCIIYALLIGPLF 170  
QY 196 GFLLAGIGDQIGTIFGKSIARVEKVFRRKQVQSKIRVISTILFILACIVFVPIPAVIF 255  
Db 171 GFLLAGVGDQIGTIFGKIAKVEDTFIKWVVSQTKIRIISTIIIFLFCVLFVALPAVIF 230  
QY 256 KYIEGNTALESIFYVWVLTTLTVGDFVAGGNAGINREWKPLVWFVILVGLAYFAAVL 315  
Db 231 KHIEGWSALDAIFYVWVLTTLTVGDFVAGG-SIEYLDYFKPVVWFVILVGLAYFAAVL 289  
QY 316 SMIGDMLRVLSKTKKEEVEGEIKAAAEKAWKANTVAETFRTRRLSVIEHDKLORATIRSM 375  
Db 290 SMIGDMLRVLSKTKKEEVEGEFRAAAEAWTANVTAETFRTRRLSVIEYDKQRTSV--- 346  
QY 376 ERRRLGLDORAHSLDMLSPKRSV 399  
Db 347 -KRKLSAELAGNHQELTPCRRTL 369

RESULT 15  
AAE28497  
ID AAE28497 standard; protein; 411 AA.  
AC AAE28497;  
DT 12-OCT-1999 (first entry)  
DE Mouse h-TREK1 polypeptide.  
XX h-TREK1; two pore potassium channel; inflammatory disease;  
KW chromosome 1q32.  
OS Mus musculus.  
PN WO9937762-A1.  
XX 29-JUL-1999.  
XX 02-DEC-1998; 98WO-EP007805.  
XX 27-JAN-1998; 98EP-00300570.  
PR 09-OCT-1998; 98GB-00022135.  
XX (SMK ) SMITHKLINE BEECHAM PLC.  
XX Meadows HJ, Chapman CG;  
PI WPI; 1999-469126/39.  
DR N-PSDB; AAZ00040.  
XX New two pore potassium channel used for, e.g. treatment of cancer,  
PT pulmonary, cardiovascular and inflammatory diseases.  
XX Claim 3; Page 26; 44pp; English.  
CC This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1  
CC polynucleotide AAZ00040. h-TREK1 is a two pore potassium channel. The  
CC polynucleotide sequence of h-TREK1 can be used to diagnose a disease or  
CC susceptibility to a disease related to expression or activity of h-TREK-1  
CC polypeptides. The methods of diagnosis may be used in the treatment of  
CC diseases including cancer, pulmonary, cardiovascular, and inflammatory  
CC diseases, pain, psychiatric disorders including depression and  
CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,  
CC and head trauma and neurological disorders including migraine



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OM protein - protein search, using sw model

Run on: June 29, 2004, 18:11:42 ; Search time 18 seconds  
(without alignments)  
1556.319 Million cell updates/sec

Title: US-09-892-360-2

Perfect score: 2760

Sequence: 1 MFELYTDFLSLVAVPAAP.....IPTDTKDRFPENNSLLDRN 538

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2760	100.0	538	1	CIWA HUMAN
2	2560.5	92.8	538	1	CIWA RAT
3	1251.5	45.3	411	1	CIW2 MOUSE
4	1218.5	44.1	426	1	CIW2 HUMAN
5	812.5	29.4	393	1	CIW4 HUMAN
6	790	28.6	398	1	CIW_MOUSE
7	512	18.6	309	1	CIW5 HUMAN
8	483	17.5	499	1	CIW5 HUMAN
9	403	14.6	336	1	CIW5 HUMAN
10	392	14.2	332	1	CIW6 HUMAN
11	390.5	14.1	336	1	CIW1 MOUSE
12	352.5	12.8	409	1	CIW3 MOUSE
13	352.5	12.8	411	1	CIW3 RAT
14	350.5	12.7	365	1	CIW9 CAVPO
15	349.5	12.7	394	1	CIW3 HUMAN
16	348.5	12.6	318	1	CIWF RAT
17	334	12.1	374	1	CIW9 HUMAN
18	333.5	12.1	313	1	CIW6 HUMAN
19	329	11.9	330	1	CIWF_HUMAN
20	326	11.8	1001	1	ORX1 DROME
21	321	11.6	237	1	CIW9 RAT
22	308	11.2	307	1	CIW8 MOUSE
23	300.5	10.9	307	1	CIW7 HUMAN
24	296.5	10.7	405	1	CIWD RAT
25	295.5	10.7	405	1	CIWD_MOUSE
26	295	10.7	408	1	CIWD_HUMAN
27	284	10.3	430	1	CIWC RAT
28	280.5	10.2	430	1	CIWC HUMAN
29	234	8.5	320	1	TWK7 CAEEL
30	217.5	7.9	691	1	TOKI YEAST
31	153.5	5.6	246	1	KCO4 ARATH
32	153.5	5.6	436	1	KCO5 ARATH
33	152	5.5	408	1	KCO3 ARATH

34	151.5	5.5	443	1	KCO2 ARATH
35	140.5	5.1	363	1	KCO1 ARATH
36	136	4.9	228	1	YMS1 CAEEL
37	127	4.6	630	1	KCD2_HUMAN
38	127	4.6	630	1	KCD2_HUMAN
39	126.5	4.6	989	1	KCH1_HUMAN
40	125	4.5	630	1	KCD2_MOUSE
41	123	4.5	457	1	XYLT_LACBR
42	121.5	4.4	899	1	VARD_SCHPO
43	121	4.4	630	1	KCD2_RAT
44	119	4.3	602	1	CIK5_RAT
45	118.5	4.3	676	1	CIQ1_HUMAN

#### ALIGNMENTS

##### RESULT 1

CIWA_HUMAN	STANDARD;	PRT;	538 AA.
ID	CIWA_HUMAN	STANDARD;	PRT;
AC	P57789; Q8TDK7; Q8TDK8; Q9HB59;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).		
GN	KCNK10 OR TREK2.		
OS	Homo sapiens (Human).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RN	SEQUENCE FROM N.A. (ISOFORM A).		
RA	MEDLINE=20435789; PubMed=1080510;		
RA	Lesage P., Terrenoire C., Romey G., Lazdunski M.,		
RT	"Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple		
RT	regulations by polyunsaturated fatty acids, lysophospholipids and Gs,		
RT	Gi, and Gq protein-coupled receptors."		
RL	J. Biol. Chem. 275:28398-28405 (2000).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORMS B AND C).		
RX	MEDLINE=21896087; PubMed=11897838;		
RA	Gu W., Schlichterthorl G., Hirsch J.R., Engels H., Karschin C.,		
RA	Karschin A., Derst C., Steinlein O.K., Daut J.,		
RT	"Expression pattern and functional characteristics of two novel splice		
RT	variants of the two-pore-domain potassium channel TREK-2."		
RL	J. Physiol. (Lond) 539:657-668 (2002).		
CC	!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY		
CC	ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.		
CC	ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING		
CC	UNSATURATED FREE FATTY ACIDS.		
CC	!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).		
CC	!- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=3;		
CC	Name=A; Synonyms=TREK-2a;		
CC	Isoid=P57789-1; Sequence=Displayed;		
CC	Name=B; Synonyms=TREK-2b;		
CC	Isoid=P57789-2; Sequence=VSP_006697;		
CC	Name=C; Synonyms=TREK-2c;		
CC	Isoid=P57789-3; Sequence=VSP_006698;		
CC	!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney		
CC	and to a lower level in brain, testis, colon, and small intestine.		
CC	Isoform b is strongly expressed in kidney (primarily in the		
CC	proximal tubule) and pancreas, whereas isoform c is abundantly		
CC	expressed in brain.		
CC	!- SIMILARITY: Belongs to the two pore domain potassium channel		
CC	family.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		



```
Db 18 VAVFAAPPVCPKSAATNGH-----HPVPRLSISSRATVVARMEGASQGLQTVMKWKT 71
Qy 72 VVALFVVVVVYLTGGLVFRALBOPFESSQNTTALBKAFLRDHVCVSPQELTILQHA 131
Db 72 VVALFVVVVVYLTGGLVFRALBOPFESSQNTTALBKAFLRDHVCVSPQELTILQHA 131
Qy 132 LDADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTGGKIFCILYAIFG 191
Db 132 LDADNAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTGGKIFCILYAIFG 191
Qy 192 IPLFGFLLAGIGDGLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIP 251
Db 192 IPLFGFLLAGIGDGLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIP 251
Qy 252 AVIFKYIEGTALESIFVYVVVLTITVGDFVAGGNAGINRYEMKPLVFWMLVGLAYF 311
Db 252 AVIFKYIEGTALESIFVYVVVLTITVGDFVAGGNAGINRYEMKPLVFWMLVGLAYF 311
Qy 312 AAVLSMTIGDMLRVLSKTKKEVGEIKAHAAEWKANTVAFRETRRLSVIHDKLOAAAT 371
Db 312 AAVLSMTIGDMLRVLSKTKKEVGEIKAHAAEWKANTVAFRETRRLSVIHDKLOAAAT 371
Qy 372 IRSMERRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQBSINNRPNLRLKGPEQL 431
Db 372 IRSMERRLGLDORAHSLDMLSPKRSVFAALDTGRFKASSQBSINNRPNLRLKGPEQL 431
Qy 432 NKHQGQASBNINIKFGSTSLRLKRNKDLKKTLPEDVQKIYKTFRNYSLDDEKBEETE 491
Db 432 NKHQGQASBNINIKFGSTSLRLKRNKDLKKTLPEDVQKIYKTFRNYSLDDEKBEETE 491
Qy 492 KMCNSDMSSTAMLTDCCIQAELNGLMPTDTRDREPNNSLLEDN 538
Db 492 KMCNSDMSSTAMLTDCCIQAELNGLMPTDTRDREPNNSLLEDN 538

RESULT 3
CIW2 MOUSE
ID CIW2 MOUSE STANDARD; PRT; 411 AA.
AC P97438:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 2 (Outward rectifying potassium
DE channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+
DE channel subunit).
GN KCKN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=9157476; PubMed=9003761;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RT "Cloning, functional expression and brain localization of a novel
RT unconventional outward rectifier K+ channel.";
RL EMBO J. 15:6854-6862(1996).
RN [2]
RP REVISIONS.
RC TISSUE=Brain;
RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA Lazdunski M.;
RN [3]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
```

```
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC HIPPOCAMPUS AND CEREBELLUM.
CC -!- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC ANESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC ISOFLURANE.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC
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CC
CC -----
CC EMBL; U73488; AAC53005.2; -.
CC MGD; MGI:109366; Kcnk2.
CC DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
CC DR GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.
CC DR GO; GO:0007185; P:G-protein coupled receptor protein signalin. .; IDA.
CC DR GO; GO:0006813; P:potassium ion transport; IDA.
CC DR InterPro; IPR003280; K-channel_2pore.
CC DR InterPro; IPR001622; K-channel_pore.
CC DR PRINTS; PR01333; 2PORECHANNEL.
CC DR PRINTS; PR01499; TREKCHANNEL.
CC DR Transport; Ion transport; Ionic channel; voltage-gated channel;
CC Potassium channel; Potassium; Transmembrane; Glycoprotein.
CC FT DOMAIN 1 46
CC FT TRANSMEM 47 67
CC FT DOMAIN 129 155
CC FT TRANSMEM 157 177
CC FT DOMAIN 178 207
CC FT TRANSMEM 208 228
CC FT DOMAIN 238 268
CC FT TRANSMEM 273 293
CC FT DOMAIN 294 411
CC FT DOMAIN 338 411
CC FT DOMAIN 354 411
CC FT CARBOHYD 95 95
CC FT CARBOHYD 119 119
CC FT SEQUENCE 411 AA; 45297 MW; 8F976DD103EFA05 CRC64;
CC
CC Query Match 45.3%; Score 1251.5; DB 1; Length 411;
CC Best Local Similarity 64.3%; Pred. No. 1.9e-69;
CC Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;
Qy 17 AAAPVCQPKSATNGQFPAPAPPTPTPLRSLSSRATVVA-RMEGTSGGGLQTVMKWTVVAI 75
Db 2 AAPDLLDPKSA-----AQNSKPRLSFSKPTVLASRVESDS---AINVMKWTVSTI 50
Qy 76 FVVVVVYLTGGLVFRALBOPFESSQNTTALBKAFLRDHVCVSPQELTILQHA 135
Db 51 FLVVVYLTGGLVFRALBOPFESSQNTTALBKAFLRDHVCVSPQELTILQHA 110
Qy 136 NAGVSPIGNSSNNSHWDLGSAFFAGTGTITTYGNIAPSTGGKIFCILYAIFG 195
Db 111 NAGIPLGNSSNNQVSHWDLGSSFFAGTGTITTYGNIAPSTGGKIFCILYAIFG 170
Qy 196 GFLLAGIGDGLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIP 255
Db 171 GFLLAGVSDGLGTIFGKSIARVEKVRKQVSTKIRVISTILFILAGCIVFTIP 230
Qy 256 KYIEGWTALESIYFVYVVVLTITVGDFVAGGNAGINRYEMKPLVFWMLVGLAYFAVL 315
Db 231 KHIEGWSALDAIFYFVYVVVLTITVGDFVAGG-SDIEYLDFFKPVVFWMLVGLAYFAVL 289
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QY 316 SMIGDLRLVSKTKEEYGEIKAHAAEWKANTVAEFRETRRLSVEIHDKLOAAATIRSM 375  
 DB 290 SMIGDLRLVSKTKEEYGEIYFAHAAEWKANTVAEFRETRRLSVEIYDFQRATSV--- 346  
 QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399  
 DB 347 -KRKLSAELAGNHQELTPCRRTL 369

RESULT 4  
 ID CIW2 HUMAN STANDARD; PRT; 426 AA.  
 AC O95069; Q9UNE3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium  
 DE channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore  
 DE potassium channel TPKC1).  
 GN KCNK2 OR TREK1 OR TREK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=99254548; PubMed=10321245;  
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;  
 RA "Inhalational anesthetics activate two-pore-domain background K+  
 RT channels".  
 RL Nat. Neurosci. 2:422-426(1999).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Brain;  
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;  
 RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS  
 CC CHLOROFORM, HALOTHANE AND ISOFLURANE.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC  
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 CC  
 CC EMBL; AF129399; AAD47569.1; -;  
 CC DR EMBL; AF004711; AAD01203.1; -;  
 CC DR Genbank; HGNC:6277; KCNK2.  
 CC DR MIM; 603219; -;  
 CC DR GO; GO:0016020; C:membrane; NAS.  
 CC DR GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.  
 CC DR GO; GO:0006813; P:potassium ion transport; NAS.  
 CC DR InterPro; IPR003280; K+channel\_2pore.  
 CC DR InterPro; IPR001622; K+channel\_pore.  
 CC DR InterPro; IPR003976; Trek channel.  
 CC DR PRINTS; PR01333; 2POREKCHANEL.  
 CC DR PRINTS; PR01499; TREKCHANNEL.  
 CC DR Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 CC Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 KW DOMAIN 1 61 CITOPLASMIC (POTENTIAL).  
 FT TRANSMEM 62 82 POTENTIAL.  
 FT DOMAIN 144 170 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 172 192 POTENTIAL.  
 FT DOMAIN 193 223 CITOPLASMIC (POTENTIAL).  
 FT TRANSMEM 224 244 POTENTIAL.  
 FT DOMAIN 253 283 PORE-FORMING 2 (POTENTIAL).  
 FT

FT TRANSMEM 288 308 POTENTIAL.  
 FT DOMAIN 309 426 CITOPLASMIC (POTENTIAL).  
 FT DOMAIN 378 426 ESSENTIAL FOR CHLOROFORM AND HALOTHANE  
 FT SENSITIVITY (BY SIMILARITY).  
 FT REQUIRED FOR BASAL CHANNEL ACTIVITY (BY  
 FT SIMILARITY).  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 2 16 MISSING (IN REF. 2).  
 FT CONFLICT 309 311 RLV -> DWL (IN REF. 2).  
 FT CONFLICT 391 391 S -> N (IN REF. 2).  
 FT CONFLICT 411 411 A -> T (IN REF. 2).  
 SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;  
 Query Match 44.1%; Score 1218.5; DB 1; Length 426;  
 Best Local Similarity 62.8%; Pred. No. 2e-67;  
 Matches 241; Conservative 58; Mismatches 68; Indels 17; Gaps 5;  
 QY 17 AAPVCPQPSATNGPPAPPTPTRLSISSTATVVA-RMECTSQGLQTVMKWTWVAI 75  
 DB 17 AAPDLDPKSA-----AQSKPRLSESTKPTVLGRVSEDT---TINVMKWTVSTI 65  
 QY 76 FVVVVVLTGGLVFRALFQPFSSQKNTIALEKAEFLRDHVCVSPQELTILQHALDAD 135  
 DB 65 FLVVVLYLIIGATVFKALEQPEHEISQRTTIVIKQTFISQHSVNSTELDELIQIVAAI 125  
 QY 136 NAGVSPIGNSNNSHWDLGSAFFAGTIVITIGVNTAPSTEGKIFCIILYAIIGIPLF 195  
 DB 126 NAGIIPLGNTSQISHWDLGSSFFAGTIVITIGFNTSPRTGKIFCIILYAIIGIPLF 185  
 QY 196 GFLLAGIGDQLTIFGKSIARVEKVKVRSQTKIRVISTILFILAGCIVFTIPAVIF 255  
 DB 186 GFLLAGVGDQLTIFGKGIKVEDTIFKWNVSQTKIRIISTIFILFGCVLFPALPIF 245  
 QY 256 KYIEGWTALESIYFVVVLTITVFGDFVAGNAGINREWKYKPLVFWILVGLAYFAAVL 315  
 DB 246 KHIEGWSALDAIVFVVITITIGFDGVAGG-SDIEYLDYFKVPVFWILVGLAYFAAVL 304  
 QY 316 SMIGDLRLVSKTKEEYGEIKAHAAEWKANTVAEFRETRRLSVEIHDKLOAAATIRSM 375  
 DB 305 SMIGDLRLVSKTKEEYGEIYFAHAAEWKANTVAEFRETRRLSVEIYDFQRATSV--- 361  
 QY 376 ERRRLGLDQRAHSLDMLSPKRSV 399  
 DB 362 -KRKLSAELAGNHQELTPCRRTL 384

RESULT 5  
 ID CIW4 HUMAN STANDARD; PRT; 393 AA.  
 AC Q9NYG8; Q96T94;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 4 (Twik-related arachidonic acid-  
 DE stimulated potassium channel protein) (TRAAK) (Two pore K+ channel  
 DE K74.1).  
 DE K74.1.  
 GN KCNK4 OR TRAAK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=20499203; PubMed=11042359;  
 RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,  
 RA Kelsall R.E., Muddock P.R., Randall A.D., Rennie G.I., Gloger I.S.;  
 RT "Cloning, localisation and functional expression of a novel human,  
 RL cerebellum specific, two pore domain potassium channel".;  
 RN Brain Res. Mol. Brain Res. 82:74-83(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RP





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CC CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC -----
DR EMBL; AF056492; AAC0481.1; -.
DR MGD; MGI:1298234; Kcnk4.
DR InterPro; IPR003280; K-channel_2pore.
DR InterPro; IPR001622; K-channel_pore.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1691; TRAAKCHANNEL.
KW Potassium channel; Potassium; Transmembrane; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 3 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 4 24 POTENTIAL.
FT DOMAIN 89 113 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 119 139 POTENTIAL.
FT DOMAIN 140 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 POTENTIAL.
FT DOMAIN 198 222 PORE-FORMING 2 (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 256 398 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPPLIC 63 67 KILVE -> KAMAI (in isoform 2).
FT FTId=VSP_006690.
FT VARSPPLIC 58 398 Missing (in isoform 2).
FT FTId=VSP_006691.
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7AEFC92 CRC64;

Query Match 28.6%; Score 790; DB 1; Length 398;
Best Local Similarity 51.9%; Pred. No. 2.7e-41;
Matches 152; Conservative 55; Mismatches 80; Indels 6; Gaps 3;

QY 67 MKKVTVAIFVVVYLTGVLVFRALQPPESQKNTIALEKAEFLADHVCVSPQLET 126
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MRSTTLALALVLLVYSGALVFOALQEPHEQQAQKMDHGRDQFLRDHPFCVSKSLED 60
QY 127 LIQHALLADNAGVSP---IGNSSNNSHWDLSGAPFPAGTVITTIYGYNIAPSTEGGKIF 183
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 FIKLVLEALGGANPETSWTNSNNSHAWNLSGAPFSGTITTIYGVNIVLHTDAGELP 120
QY 184 CILYAFGPIPLFGLLAGIGDQGLTFGKSIARVEKVFVKQVSTKIRVISTILFILAG 243
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 CIFVALVGPIPLFGLLAGVDRGLSSLRGICIEAIFLKHVPFPLVRSLSAVLFLIG 180
QY 244 CIVFTIIPAVFKYTEGTALESIFVYVVTITVTGFGDFVAGGNAGINREMYKPLAWFW 303
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 CLLVLTITTFVFSYMESKLEAIFVILVITVTGFGDYPDGTGQN-SPAYPLVWFVW 239
QY 304 ILVGLAYFAVLNMTGDWLRLVLSKTKKEVEGEIKAHAAEWKANYTAPEFTRR 356
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
240 ILFGLAYFASVLTITIGNWLAVRSRTRAEAGMGLTAQAASGTGTVA--RVTOR 290

RESULT 7
CIWG HUMAN
ID CIWG HUMAN STANDARD; PRT; 309 AA.
AC Q96T55; Q9H591;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-VAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 16 (TWIK-related alkaline pH
DE activated K+ channel 1) (2P domain potassium channel Taik-1).

```

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GN KCKN16 OR TALK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=21164727; PubMed=11263999;
RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA Lazdunski M., Lesage F.;
RT "Genomic and functional characteristics of novel human pancreatic 2P
RT domain K(+) channels.";
RL Biochem. Biophys. Res. Commun. 282:249-256(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Williams S.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly
CC activating and non-inactivating outward rectifier K(+) currents.
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96T55-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96T55-2; Sequence=VSP_006699;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in pancreas.. Not detectable
CC in the other tissues tested.
CC -!- MISCELLANEOUS: Inhibited by Ba(+2), quinine, quinidine, chloroform
CC and halothane. Activated at alkaline pH.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.
CC -----
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CC -----
DR EMBL; AF358909; AAK49532.1; -.
DR EMBL; ALI36087; CAC07336.1; -.
DR Genew; HGNC:14464; KCKN16.
DR MIM; 607369; -.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003092; TASK_channel.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
DR Transport; Ion transport; Ionic channel; Voltage-gated channel;
DR Potassium channel; Potassium; Transmembrane; Alternative splicing.
KW DOMAIN 1 13 POTENTIAL.
KW TRANSMEM 14 34 PORE-FORMING 1 (POTENTIAL).
KW DOMAIN 98 116 POTENTIAL.
KW TRANSMEM 120 140 CYTOPLASMIC (POTENTIAL).
KW DOMAIN 141 165 POTENTIAL.
KW TRANSMEM 166 186 PORE-FORMING 2 (POTENTIAL).
KW DOMAIN 202 221 POTENTIAL.
KW TRANSMEM 238 258 CYTOPLASMIC (POTENTIAL).
KW DOMAIN 259 309 LROGGGAKAAGRRRRGSGTAARGVQVTPDEPIKKGILGS
KW VARSPPLIC 269 309 -> RGLGVKDGASPSGLPRQKIPISA (in isoform
KW 2).
SQ SEQUENCE 309 AA; 34153 MW; 99C4B1EB26B0764 CRC64;

Query Match 18.6%; Score 512; DB 1; Length 309;
Best Local Similarity 40.2%; Pred. No. 1.9e-24;
Matches 99; Conservative 55; Mismatches 86; Indels 6; Gaps 3;

```

QY 72 VVAIFVVVVVYVTGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQSELETIQLIQA 131  
 Db 14 VLPLLLAYCYLLGATIGFOLLERQAEQSRDQFQLEKLFLENYTCLDQWAMEQFVQVI 73  
 QY 132 LDADNAGVPIGNSSNNSHWDLGSFAFFAGTVITTIIGYNTAPSTEGKIFCIYLAIFG 191  
 Db 74 MEAWVGVNPKGNST-NPSNWDPSGFFAGTVITTIIGYNTAPSTEGKIFCIYLAIFG 132  
 QY 192 IPIFGFLLAGIGDQGLTIFGKSIARVEKVRKQVSTQKIRVISTITLFLAGCIVFVTIP 251  
 Db 133 IPLNVIFL---NHLGTGLRAHLAATERWEDRRRSQV-LQVLGLALFTLTGLTVLIFP 187  
 QY 252 AVTKIEGHTALESYFVVVITVTGFGDFVAGNAGINREYKPLVWFVILVGLAYF 311  
 Db 188 PMVFSHVEGVSFSGFYFAFIFLTITLSTIGFGDVVVGTPSKHYISVYRSALAIWILLGLAWL 247  
 QY 312 AAVLSM 317  
 Db 248 ALILPL 253

RESULT 8  
 CIW5\_HUMAN STANDARD; PRT; 499 AA.  
 AC 095279;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 5 (Acid-sensitive potassium channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).  
 GN KCNK5 OR TASK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=99030343; PubMed=9812978;  
 RA Reyes R.; Duprat F.; Lesage F.; Fink M.; Salinas M.; Farman N.; Lazdunski M.  
 RT "Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney."  
 RL J. Biol. Chem. 273:30863-30869(1998).  
 CC -!- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL K+ CONCENTRATIONS.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.  
 CC -!- MISCELLANEOUS: INHIBITED BY QUININE, QUININDINE AND EXTERNAL ACIDIFICATION.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel family.  
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 CC -----  
 CC EMBL; AF084830; AAC79458.1; -.  
 CC Genbank; HGNC:6280; KCNK5.  
 CC MIM; 603493; -.  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0005267; F:potassium channel activity; TAS.  
 CC GO; GO:0007588; P:excretion; TAS.

GO; GO:0006813; P:potassium ion transport; TAS.  
 DR InterPro; IPR003280; K:channel\_2pore.  
 DR InterPro; IPR001622; K:channel\_pore.  
 DR InterPro; IPR003092; TASK\_channel.  
 DR PRINTS; PR01333; 2PORECHANNEL.  
 DR PRINTS; PR01095; TASKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel; Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 7 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 8 26 POTENTIAL.  
 FT DOMAIN 85 112 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT DOMAIN 134 157 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 158 180 POTENTIAL.  
 FT DOMAIN 190 215 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 230 250 POTENTIAL.  
 FT DOMAIN 251 325 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 77 N-LINKED (GLCNAC..) (POTENTIAL).  
 SQ SEQUENCE 499 AA; 55130 MW; E871A7A4823DDA00 CRC64;

Query Match 17.5%; Score 483; DB 1; Length 499;  
 Best Local Similarity 25.8%; Pred. No. 2e-22;  
 Matches 131; Conservative 81; Mismatches 185; Indels 110; Gaps 14;

QY 79 VVYLVTVGLVFRALQPFSSQKNTIALEKAEFLRDHVCVSPQSELETIQLIHALDADNAG 138  
 Db 12 IIFYLALGAALFEVLEESPHWKEAKNYVTQKLHLKEPFCGLQEGDLKILEWSDAAGQG 71  
 QY 139 VSPIGNSSNNSHWDLGSFAFFAGTVITTIIGYNTAPSTEGKIFCIYLAIFGIFLFGFL 198  
 Db 72 VAITGNQTFN--NMWPNAMIFAATVITTIIGYNAVAPKTPAGRLFCVYFGLFVPL----C 126  
 QY 199 LAGIGDQGLTIFGKSIARVEKVRKQVSTQKIRVISTITLFLAGCIVFVTIPVIFKYI 258  
 Db 127 LTWL-SALGKPFGGPAKELGQFLTKRGVSLKAQITCTVIFVGVLVHLVPPFVMT 185  
 QY 259 EGTWALESIYFVVVITVTGFGDFVAGNAGINREYKPLVWFVILVGLAYFAVLMSI 318  
 Db 186 EGNWYIEGLYSFITISTIGFGDFVAGVNPNSANYHALYRYFVFWIYLGLA----- 236  
 QY 319 GDLRLVLSKTKKEVEGEIKAAHAEKNAVTAFTRETRRLSVEIHDKLQRAATIRSMERR 378  
 Db 237 --WLSLF-----VNWKVS-----MEVEVHKAIK-----KRRRR 263  
 QY 379 RLGLDQRAHSLDMLSPKRSVFAALDTGRFKASQESINNNPNLRLK-----GP 428  
 Db 264 KESPESSPHSRKALQVKGSTASKDVNIFSLSKKEETYNDLIKQIGKKAMKTSGGGETGP 323  
 QY 429 -EQLNKHGQG-----ASEDNIINKFGSTSLTKRKNKDLKXTLPED 468  
 Db 324 GPGLPQGGGUPALPPLVPLVYVSKNRPVPLEEVSTQLRSKGVRSRSPDEAVARAPED 383  
 QY 469 VQKIYKTFRTNYSLDDEEKKEE-----TERKMCNDSNSTAMLTDC 507  
 Db 384 SSPAPEVFMV-QLDRISECEPMDAQDYHPLIFQDASITFVNTTEAGLSDEETSKSLEDN 442  
 QY 508 I-----QCHAS-----LENGHPIPTDK 524  
 Db 443 LAGEESPQGAERAKAPLNNGEFPSSSE 469

RESULT 9  
 CIW1\_HUMAN STANDARD; PRT; 336 AA.  
 ID CIW1\_HUMAN  
 AC 000180; Q13307;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (Inward rectifying potassium channel protein TWIK-1) (Potassium channel KCNOL).  
 GN KCNK1 OR TWIK1 OR HOH01 OR KCNOL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.  
 RC TISSUE=Kidney;  
 RC MEDLINE=96183184; PubMed=8605869;  
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,  
 RA Barhanin J.;  
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K<sup>+</sup> channel with a  
 RT novel structure";  
 RL EMBO J. 15:1004-1011(1996).  
 RN [2]  
 RN SEQUENCE FROM N.A., AND REVIEW.  
 RN TISSUE=Brain;  
 RC MEDLINE=98122696; PubMed=9462864;  
 RA Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;  
 RT "Sequence and function of the two P domain potassium channels:  
 RT implications of an emerging superfamily";  
 RL J. Mol. Med. 76:13-20(1998).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC MEDLINE=98026667; PubMed=9362344;  
 RA Orlas M., Velazquez H., Tung F., Lee G., Desir G.V.;  
 RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive  
 RT expression in distal nephron segments";  
 RL Am. J. Physiol. 273:F663-F666(1997).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RC MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin N.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Cunnatne P.H.,  
 RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heltan E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schneringer A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Weakly inward rectifying potassium channel.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Widely expressed with high levels in heart and  
 CC brain and lower levels in placenta, lung, liver and kidney.  
 CC -!- MISCELLANEOUS: Inhibited by barium, quinine, quinidine and  
 CC internal acidification. Activated by protein kinase C.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; U33632; AAB01688.1; -;  
 DR EMBL; U76996; AAB97878.1; -;  
 DR EMBL; U90065; AAB51147.1; -;  
 DR EMBL; BC018051; AAB18051.1; -;  
 DR PIR; S65566; S65566.

DR Genew; HGNC:6272; KCNK1.  
 DR MIM; 601745; -;  
 DR GO; GO:0008076; C-voltage-gated potassium channel complex; TAS.  
 DR GO; GO:0005242; F-inward rectifier potassium channel activity; TAS.  
 DR GO; GO:0006813; P-potassium ion transport; TAS.  
 DR InterPro; IPR003280; K-channel\_2pore.  
 DR InterPro; IPR016322; K-channel\_pore.  
 DR InterPro; IPR001779; TWIK1 channel.  
 DR InterPro; IPR005408; TWIK channel.  
 DR PRINTS; PR01333; 2POREKCHANEL.  
 DR PRINTS; PR01096; TWIKCHANNEL.  
 DR PRINTS; PR01586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 133 133 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT MUTAGEN 161 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.  
 SQ SEQUENCE 336 AA; 38143 MW; 2A41D9501323215D CRC64;  
 Query Match 14.6%; Score 403; DB 1; Length 336;  
 Best Local Similarity 33.2%; Pred. No. 9.6e-18;  
 Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;  
 QY 76 FVVV--VVVLTGGLVFRALRQPFSSQKNTTALSKAEFLRDHVCVSQDELTLQHALD 133  
 DB 25 FLVLGGLLYLVFGAVVFSFVPELDLRLQELKRLRFLSEHECLSEQQEQLGRVLE 84  
 QY 134 ADNAGVSPICNSNNKSHWDLGSAFFAGTAVTTTGYGNIAPSTGGKIFCILYAFIGIP 193  
 DB 85 ASNYGVSVLSNAGN-WNWDFTSALFPASTVLSTTGYGHTVPLSDGKAFCLIIYSVIGIP 143  
 QY 194 LFGFLIAGIGDGLTIFGKSIARVSKVPRKKQV-----SQTIRVISTIL--FILA 242  
 DB 144 FTLELTAV-----VQRITVHTVRRLVYFHIRWGFSKQVAIVHAVLLGFVTV 192  
 QY 243 GCIVFVTIPAVIFKYIE-GWTALESIIYFVWLTGFGDFVAGNAGINREMYKPLVM 301  
 DB 193 SCFFP--IPAAVFSVLEDDWNPLESFYFCFTLSLTIGLDVYPGEGYNQKRELYKIGIT 250  
 QY 302 FWLVGLAYFAAVLSMIGDLRLVLSK-----KTKEVEGEIKAHAAE 342  
 DB 251 CYLLGLIAMLVLETFCF-LHELKKFKRMFVKKDKDQVHTE 295  
 RESULT 10  
 ID CIWH HUMAN STANDARD; PRT; 332 AA.  
 AC Q96754; Q8TAW4; Q9BXD1; Q9H592;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 17 (TWIK-related alkaline pH  
 DE activated K<sup>+</sup> channel 2) (2P domain potassium channel Talk-2) (TWIK-  
 DE related acid-sensitive K<sup>+</sup> channel 4) (TASK-4).  
 GN KCNK17 OR TALK2 OR TASK4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Pancreas;  
 RX MEDLINE=21164727; PubMed=11263999;  
 RA Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,  
 RA Lazdunski M., Lesage F.;

RT "Genomic and functional characteristics of novel human pancreatic 2P  
 RT domain K(+) channels.";  
 RL Biochem. Biophys. Res. Commun. 282:249-256(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Adrenal gland;  
 RX MEDLINE=21145510; PubMed=11248242;  
 RA Decher N., Maier M., Ditttrich W., Gassenhuber J., Brueggemann A.,  
 RA Busch A.E., Steinmeyer K.;  
 RT "Characterization of TASK-4, a novel member of the pH-sensitive,  
 RT two-pore domain potassium channel family.";  
 RL FEBS Lett. 492:84-89(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RA Williams S.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Lung and Spleen;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Klausberger R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Atschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly  
 CC activating and non-inactivating outward rectifier K(+) currents.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q96T54-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q96T54-2; Sequence=VSP\_006700;  
 CC Note=No experimental confirmation available;  
 CC -!- MISCELLANEOUS: Inhibited by Ba(+2), quinidine, chloroform and  
 CC halothane. Activated at alkaline pH. Activated by quinine and  
 CC isoflurane.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel  
 CC family.  
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous  
 CC gene model prediction.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AF358910; AA49533.1; -;  
 CC EMBL; AF339912; AA28551.1; -;  
 CC EMBL; AL136087; CA07335.1; ALT\_SEQ.  
 CC EMBL; BC025726; AAC25726.1; -;  
 CC Genew; HGNC:14465; KCNK17.  
 CC MIM; 607370; -;

DR InterPro; IPR003280; K+channel\_2pore.  
 DR InterPro; IPR001622; K+channel\_pore.  
 DR InterPro; IPR003092; TASK channel.  
 DR PRINTS; PRO1333; 2POREKCHANEL.  
 DR PRINTS; PRO1095; TASKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel;  
 KW Potassium channel; Potassium; Transmembrane; Glycoprotein;  
 KW Alternative splicing.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 43 POTENTIAL.  
 FT DOMAIN 106 124 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 128 148 POTENTIAL.  
 FT DOMAIN 149 179 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 180 200 POTENTIAL.  
 FT DOMAIN 211 230 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 244 264 POTENTIAL.  
 FT DOMAIN 265 332 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 265 332 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 94 94 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT VARSPLIC 260 332 IKLLISOLETPGRVSCCHHSKEDFKSQNRQGGDPREPES  
 FT PSWRRQGGYVPAATLAKTSIPKAGDRDLTGSGQSPFHSK  
 FT DAIQDPWESYSIWNLLTLQAVARTASYTPFFGSRPR  
 FT (in isoform 2).  
 FT /FTId=VSP\_006700.  
 FT CONFLICT 21 21 S -> G (IN REF. 2 AND 4).  
 FT SEQUENCE 332 AA; 36894 MW; 1848DBC06E078158 CRC64;  
 Query Match 14.2%; Score 392; DB 1; Length 332;  
 Best Local Similarity 31.2%; Pred. No. 4.4e-17;  
 Matches 85; Conservative 59; Mismatches 114; Indels 14; Gaps 3;  
 QY 47 SRATVAVMEGTSQGLQTVMKKTVAIFVVVVVYVTGLVFRALROPFESSQKNTIA 106  
 DB 6 ARAAEGRVRCGV-----PSTVLLLAYLAYLALGTGVFTLGRRAQDSRSFQ 56  
 QY 107 LEKAEFLRDHVCVSPQELTLIQHALDADNAGVSPIGNSSNNSSHDLSGAPFFAGTVIT 166  
 DB 57 RDKWELLQNTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115  
 QY 167 TTGYGNAPISPEGKIFCLVAFIPFLFGFLLAGIGDQLGTIFGKSTARVEKVKKQV 226  
 DB 116 TIGYGNLSPNTWAARLFCIFVALVGIPLNVLVVL-----NRLGHLMOQGVNHWASRLGGTQV 171  
 QY 227 SQTIRVSTILFILAGCIVFTIPAVIFKFTIEGWTALLESIVFVVVTLTTVFGSDFVAGG 286  
 DB 172 DFDKARWLAGSGALLSGLLFLPLPFLFSMEGVSYTEGFYFAFITLSTVGFGDYVIGM 231  
 QY 287 NAGINRYREWKPLVFWFVILVGLAYFAVLSMI 318  
 DB 232 NPSQRYPLWKYKNVSLWILFGWALIALIKLI 263  
 RESULT 11  
 CIWI\_MOUSE STANDARD; PRT; 336 AA.  
 ID CIWI\_MOUSE AC 008581;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 1 (Inward rectifying potassium  
 DE channel protein TWIK-1).  
 GN KCNK1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97165959; PubMed=9013852;  
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,  
 RA Lazdunski M.;

RT "The structure, function and distribution of the mouse TWIK-1 K+ channel.";  
 RL FEBS Lett. 402:28-32(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Liver;  
 RX MEDLINE=98218573; PubMed=9559671;  
 RA Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;  
 RT "Structure, chromosome localization, and tissue distribution of the mouse Twik K+ channel gene";  
 RL FEBS Lett. 425:310-316(1998).  
 CC -!- FUNCTION: Weak inwardly rectifying potassium channel.  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: Widely expressed. Highest expression in brain, kidney, thyroid, salivary gland, adrenal gland, prostate, epididymis, uterus, placenta, colon and jejunum. Moderate expression in eyes, pituitary, pancreas, smooth muscle, testis and ovary. Very low levels in lung, aorta, liver, heart, skeletal muscle, thymus and spleen. In the brain, highest expression in cerebellar granule cells, brainstem, hippocampus and cerebral cortex.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND STABILIZES AFTER DAY 8.  
 CC -!- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel family.  
 CC -----  
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 CC -----  
 CC EMBL; AF033017; AAC16973.1; -;  
 DR MGD; MGI:109322; Kcnk1.  
 DR InterPro; IPR003280; K+channel 2pore.  
 DR InterPro; IPR001622; K+channel pore.  
 DR InterPro; IPR001779; TWIK1 channel.  
 DR InterPro; IPR005408; TWIK Channel.  
 DR PRINTS; PR01333; 2PORECHANEL.  
 DR PRINTS; PR01096; TWIKCHANNEL.  
 DR PRINTS; PR01586; TWIKCHANNEL.  
 KW Transport; Ion transport; Ionic channel; Voltage-gated channel; Potassium channel; Potassium; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 POTENTIAL.  
 FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).  
 FT TRANSMEM 133 153 POTENTIAL.  
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 178 198 POTENTIAL.  
 FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).  
 FT TRANSMEM 247 267 POTENTIAL.  
 FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 95 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 336 AA; 38275 MW; A996060A18266FD4 CRC64;  
 Query Match 14.1%; Score 390.5; DB 1; Length 336;  
 Best Local Similarity 33.7%; Pred. No. 5.6e-17;  
 Matches 94; Conservative 49; Mismatches 99; Indels 37; Gaps 9;  
 QY 76 FVVV-VVYLVYGVVFPALQPESSQXNTIALEKAEFLDHVCVSPQLETLIQHALD 133  
 DB 25 FLVGYLLVYGVVFPALQPESSQXNTIALEKAEFLDHVCVSPQLETLIQHALD 84  
 QY 134 ADNAGVSPIGNSSNNSHWDIGSFAFFAGTVITIGYGNIAPEPGEKIFCIYAIYFIP 193  
 DB 85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLTSTGTGHTVLTSLSDGKGKCIYVIGIP 143

QY 194 LFGLLAGIGDQLGTFGKSIARVEKVRKQV-----SQTQKIRVISITL--FILA 242  
 DB 144 FTLLFTAL-----VQRTVTHVTRPVLVYFHIRWGSQVVAIVHVALLGFTV 192  
 QY 243 GCIVFVTPPAVIFKYIE-GWTALESYIFVVTITVVGDFGVAGNAGINREYWKPLVW 301  
 DB 193 SCFF--IPAAVFSVLEDDNFLESFYFCFISLTIGLDGYVPGEGYNOKFRELYKIGT 250  
 QY 302 FWLVGLAYFAAVLSMIGDMLRVL-----KTKKEE 332  
 DB 251 CYLLGLITMLVLETFCE-LHELKFKRMVYKKDKDE 288

RESULT 12  
 C1W3 MOUSE STANDARD; PRT; 409 AA.  
 ID C1W3\_MOUSE  
 AC Q351L1; Q35163;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)  
 DE (Cardiac two-pore background K+ channel) (CTBAK-1) (Two pore potassium channel KT3.1)  
 DE channel KT3.1)  
 GN KCNK3 OR TASK1 OR TASK OR CTBAK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=98165556; PubMed=9506712;  
 RA Kim D., Fujita A., Horio Y., Kurachi Y.;  
 RT "Cloning and functional expression of a novel cardiac two-pore background K+ channel (CTBAK-1).";  
 RL Circ. Res. 82:513-518(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=20287574; PubMed=10748056;  
 RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;  
 RT "Proton block and voltage gating are potassium-dependent in the cardiac leak channel Kcnk3";  
 RL J. Biol. Chem. 275:16969-16978(2000).  
 RN [3]  
 RP SEQUENCE OF 4-409 FROM N.A.  
 RX MEDLINE=97459932; PubMed=9312005;  
 RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;  
 RT "TASK, a human background K+ channel to sense external pH variations near physiological pH";  
 RL EMBO J. 16:5464-5471(1997).  
 CC -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD (BY SIMILARITY).  
 CC -!- SUBUNIT: Homodimer (Potential).  
 CC -!- TISSUE SPECIFICITY: Integral membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.  
 CC -!- MISCELLANEOUS: INACTIVATED BY BARIUM.  
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel family.  
 CC -----  
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 CC -----



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QY 242 AGCIVFTIPAVIPKVIETGNTALSIYFVVVTLTVGFGDFA--GNGAGINRYREWKPLV 300
DB 165 VSCITLCIGAAAFSYERWFFQAYYFCITLTITGFGDVALQKQALQTOPOYVAFS 224
QY 301 FFWILVGLAYFAAALSMIGMDLRLVLSKTKKEEVEGEIKAKAAEWKANVT 348
DB 225 FVYIITGLTVIGAFNLV--VLRFTWNAEDKRD-----AEHRLALT 265

RESULT 14
CIW9 CAVPO STANDARD; PRT; 365 AA.
AC Q9JUL58;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
DE channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
GN KCNK9 OR TASK3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20287530; PubMed=10747866;
RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA Karschin A., Derst C.;
RT "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT extracellular histidine as pH sensor.";
RL J. Biol. Chem. 275:16650-16657(2000).
CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC family.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF212827; AAF63706.1; -
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005407; TASK3_channel.
DR InterPro; IPR003092; TASK_channel.
DR Pfam; PF00520; ion trans; 1.
DR PRINTS; PR01333; 2FOREXCHANNEL.
DR PRINTS; PR01585; TASK3CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW Potassium channel; Potassium; Transmembrane; Glycoprotein.
FT DOMAIN 1 8
FT TRANSMEM 9 29
FT POTENTIAL.
FT DOMAIN 78 101
FT TRANSMEM 108 128
FT POTENTIAL.
FT DOMAIN 129 158
FT TRANSMEM 159 179
FT POTENTIAL.
FT DOMAIN 184 207
FT TRANSMEM 219 239
FT POTENTIAL.
FT DOMAIN 240 365
FT CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 53 53
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 365 AA; 40769 MW; 261DC973FF53AF91 CRC64;

Query Match 12.7%; Score 350.5; DB 1; Length 365;
Best Local Similarity 26.9%; Pred. No. 1.7e-14;
Matches 112; Conservative 72; Mismatches 153; Indels 79; Gaps 17;

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QY 67 MKWKTV--VAIFVWVVLVTCGLVFRALQPFSSQKNTALEKAEFLRDHVCVSPQ-- 122
DB 1 MKKQNVRLSLIACTFTYLLVGAAVFDALSDHEKREBEKLAEBIR-IRKYNISTSDY 59
QY 123 -ELETLIQHALDADNAGVSPIGNSNSSHMDLGSFAFFAGTVITIGYGNIAPISTEGGK 181
DB 60 RQELVILQS-EPHEAGV-----QWKEAGSFYFAITVITIGYHAAPGTGDKG 107
QY 182 IFCILYAIPIGFLFGLLAGIGDQLGTIFGKSIARVEKV--FRKQVQTKIRVISTILF 239
DB 108 AFCMFYAVLGIPLTLVFMFQSLGERMNTFVRYLLKIKKCCGMRNTEVSMENNVTVG-- 163
QY 240 ILAGCIVFTIPAVIPKVIETGNTALSIYFVVVTLTVGFGDFAVAGNAG-INYREWKP 298
DB 164 -FFSCMTLCIGAAAFSQCEWSFFHAYYICFTLTITGFGDVALQKQALQRPFFVA 222
QY 299 LVWFILVGLAYFAAALSMIGMDLRLVLSKTKKEEVE-----IKAAHAAWKANVTAEFR 352
DB 223 FEFMVLVGLTVIGAFNLV--VLRFLTWNSDEERGEGBEGAALPGNPFSSVVTHISEAR 280
QY 353 ETRRLSVEIHD--KLQRAATIRSMERRLG---LDORAHS-----LDMLSP--KESYFA 401
DB 281 QVRQRYRGEGDLQSVCSACVRS--QPQNFATLAPQPLHSISCRIEISSTLKNLFF- 338
QY 402 ALDTGRFKASSQESINNRPNLRLKGPQLNKHGQGSADNIINKFGSTSLRTK 457
DB 339 -----PSPISVSPG-----LHSGFDNHLMLRR 362

RESULT 15
CIW3 HUMAN STANDARD; PRT; 394 AA.
AC O14649;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Potassium channel subfamily K member 3 (acid-sensitive potassium
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE (Two pore potassium channel KT3.1).
GN KCNK3 OR TASK1 OR TASK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97459932; PubMed=9312005;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
RT near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,
RX Goldstein S.A.N.;
RT "Proton block and voltage-gating are potassium-dependent in the
RT cardiac leak channel Kcnk3.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245;
RX Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [4]
RP MUTAGENESIS OF HIS-98.
RX MEDLINE=21535313; PubMed=11680614;
RX Ashmole I., Goodwin P.A., Stanfield P.R.;
RT "TASK-5, a novel member of the tandem pore K+ channel family.";

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RL Pflogers Arch. 442:828-833(2001).

CC -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM

CC CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM

CC ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN

CC OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

CC WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.

CC SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST

CC EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,

CC LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.

CC -!- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY

CC HALOTHANE AND ISOFLURANE.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel

CC family.

CC -----

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CC -----

CC EMBL; AF006823; AAC51777.1; -

CC EMBL; AF065163; AAG29340.1; -

CC Genew; HGNC:6278; KCNK3.

CC MIM; 603220; -

CC GO; GO:0005887; C: integral to plasma membrane; TAS.

CC GO; GO:0005267; F: potassium channel activity; TAS.

CC GO; GO:0006813; P: potassium ion transport; TAS.

CC GO; GO:0007268; P: synaptic transmission; TAS.

CC InterPro; IPR005821; Ion trans.

CC InterPro; IPR003280; K+channel\_2pore.

CC InterPro; IPR001622; K+channel\_pore.

CC InterPro; IPR005406; TASK1\_channel.

CC InterPro; IPR003092; TASK\_channel.

CC Pfam; PF00520; ion trans; 1.

CC PRINTS; PR01333; 2PORECHANNEL.

CC PRINTS; PR01584; TASK1CHANNEL.

CC PRINTS; PR01095; TASKCHANNEL.

CC Transprot; ion transport; Ionic channel; Voltage-gated channel;

CC Potassium channel; Potassium; Transmembrane; Glycoprotein.

CC DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 9 29 POTENTIAL.

CC DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).

CC TRANSMEM 108 128 POTENTIAL.

CC DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 159 179 POTENTIAL.

CC DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).

CC TRANSMEM 223 243 POTENTIAL.

CC DOMAIN 244 394 CYTOPLASMIC (POTENTIAL).

CC CARBOHYD 53 53 N-LINKED (GLCNAC...) (POTENTIAL).

CC MUTAGEN 98 98 H-N: GREATLY REDUCES PH SENSITIVITY.

CC SEQUENCE 394 AA; 43518 MW; 9FF4C8266F615F67 CRC64;

Query Match 12.7%; Score 349.5; DB 1; Length 394;

Best Local Similarity 32.8%; Pred. No. 2.le-14;

Matches 95; Conservative 53; Mismatches 109; Indels 33; Gaps 10;

QY 67 MKWTV--VAIFVVVVVYVVGIVFVAPPPSSOKNTIALEKAEFLRDHVCVSP---121

DB 1 MKRQNVTLALIVCTFTYLLVGAADFALSEFELIERQQLRQQLRARNLSQGGY 59

QY 122 QLEPTLIQHALDADNAGVSPIGNSSNNSSHDGLGSAPFFAGTVTTTIGYGNIPSTEGGK 181

DB 60 EELERVLR-LKPHKAGV-----QWRFAGSFYFAITVTTTIGYGAAPSTDGK 107

QY 182 IFCLLYAIFGPIPLGPILAGIDGLTIFGKSTARVEK--VFRKKQVSTQKIRVISTILF 239

DB 108 VFCMFYALLGLLPLVLMFQSLGERINTLVYLLHRAKKGLGMRADVSMANN-----VLI 162

QY 240 ILACIVFVTIPAVIFKYGIEGWTALLESITYFVVVTLTTVGFDFVA-CGNAGINRYRWYKP 298

Db 163 GFESCISTLCIGAAAFSGHYEHWTFFQAYYYCFITLTITIGFDYVALQKQALQTPQYVA 222

QY 299 LVWFWIIVGLAYFAAVLSMIGDWLRVLVSKTKSEVGEIKAHAAEWKANVT 348

Db 223 FSVYIILTGLTVIGAFNLV--VLRFTMNAEDEKRD-----AEHRALLT 265

Search completed: June 29, 2004, 18:18:24

Job time : 19 secs

